

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

(i) APPLICANT: JOHNSON, EUGENE M  
 MILBRANDT, JEFFREY D  
 KOTZBAUER, PAUL T  
 LAMPE, PATRICIA A  
 KLEIN, ROBERT  
 DESAUVAGE, FRED



(ii) TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTOR

(iii) NUMBER OF SEQUENCES: 242

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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
 (B) COMPUTER: IBM PC compatible  
 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 09/220,617  
 (B) FILING DATE: 24 Dec. 1998  
 (C) CLASSIFICATION:

E 14

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: GENDLOFF, ELIE H.  
 (B) REGISTRATION NUMBER: 44,704  
 (C) REFERENCE/DOCKET NUMBER: 6029-7976

(ix) TELECOMMUNICATION INFORMATION:

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## (2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 102 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Ala	Arg	Leu	Gly	Ala	Arg	Pro	Cys	Gly	Leu	Arg	Glu	Leu	Glu	Val	Arg
1									10					15	

Val	Ser	Glu	Leu	Gly	Leu	Gly	Tyr	Ala	Ser	Asp	Glu	Thr	Val	Leu	Phe
													20	25	30

Arg Tyr Cys Ala Gly Ala Cys Glu Ala Ala Ala Arg Val Tyr Asp Leu  
 35 40 45  
 Gly Leu Arg Arg Leu Arg Gln Arg Arg Arg Leu Arg Arg Glu Arg Val  
 50 55 60  
 Arg Ala Gln Pro Cys Cys Arg Pro Thr Ala Tyr Glu Asp Glu Val Ser  
 65 70 75 80  
 Phe Leu Asp Ala His Ser Arg Tyr His Thr Val His Glu Leu Ser Ala  
 85 90 95  
 Arg Glu Cys Ala Cys Val  
 100

## (2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 100 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Pro Gly Ala Arg Pro Cys Gly Leu Arg Glu Leu Glu Val Arg Val Ser  
 1 5 10 15  
 Glu Leu Gly Leu Gly Tyr Thr Ser Asp Glu Thr Val Leu Phe Arg Tyr  
 20 25 30  
 Cys Ala Gly Ala Cys Glu Ala Ala Ile Arg Ile Tyr Asp Leu Gly Leu  
 35 40 45  
 Arg Arg Leu Arg Gln Arg Arg Val Arg Arg Glu Arg Ala Arg Ala  
 50 55 60  
 His Pro Cys Cys Arg Pro Thr Ala Tyr Glu Asp Glu Val Ser Phe Leu  
 65 70 75 80  
 Asp Val His Ser Arg Tyr His Thr Leu Gln Glu Leu Ser Ala Arg Glu  
 85 90 95  
 Cys Ala Cys Val  
 100

## (2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: Modified-site
  - (B) LOCATION: 6
  - (D) OTHER INFORMATION: /note= "ANY AMINO ACID"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

1	5	10	15												
Ser	Gly	Ala	Arg	Pro	Xaa	Gly	Leu	Arg	Glu	Leu	Glu	Val	Ser	Val	Ser

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 10 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
  - (A) NAME/KEY: Modified-site
  - (B) LOCATION: 1
  - (D) OTHER INFORMATION: /note= "ANY AMINO ACID"

- (ix) FEATURE:
  - (A) NAME/KEY: Modified-site
  - (B) LOCATION: 6
  - (D) OTHER INFORMATION: /note= "SERINE OR CYSTEINE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

1	5	10							
Xaa	Cys	Ala	Gly	Ala	Xaa	Glu	Ala	Ala	Val

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
  - (A) NAME/KEY: Modified-site
  - (B) LOCATION: 1
  - (D) OTHER INFORMATION: /note= "ANY AMINO ACID"

- (ix) FEATURE:
  - (A) NAME/KEY: Modified-site
  - (B) LOCATION: 2
  - (D) OTHER INFORMATION: /note= "ANY AMINO ACID"

- (ix) FEATURE:
  - (A) NAME/KEY: Modified-site
  - (B) LOCATION: 17
  - (D) OTHER INFORMATION: /note= "GLUTAMINE OR GLUTAMIC ACID"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

1	5	10	15												
Xaa	Xaa	Val	Glu	Ala	Lys	Pro	Cys	Cys	Gly	Pro	Thr	Ala	Tyr	Glu	Asp

Xaa Val Ser Phe Leu Ser Val  
20

## (2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 10 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Tyr	His	Thr	Leu	Gln	Glu	Leu	Ser	Ala	Arg
1				5				10	

## (2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 197 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met	Gln	Arg	Trp	Lys	Ala	Ala	Ala	Leu	Ala	Ser	Val	Leu	Cys	Ser	Ser
1					5			10					15		

Val	Leu	Ser	Ile	Trp	Met	Cys	Arg	Glu	Gly	Leu	Leu	Leu	Ser	His	Arg
					20			25					30		

Leu	Gly	Pro	Ala	Leu	Val	Pro	Leu	His	Arg	Leu	Pro	Arg	Thr	Leu	Asp
						35		40			45				

Ala	Arg	Ile	Ala	Arg	Leu	Ala	Gln	Tyr	Arg	Ala	Leu	Gln	Gly	Ala
					50		55			60				

Pro	Asp	Ala	Met	Glu	Leu	Arg	Glu	Leu	Thr	Pro	Trp	Ala	Gly	Arg	Pro
					65		70		75			80			

Pro	Gly	Pro	Arg	Arg	Ala	Gly	Pro	Arg	Arg	Arg	Ala	Arg	Ala
					85		90		95				

Arg	Leu	Gly	Ala	Arg	Pro	Cys	Gly	Leu	Arg	Glu	Leu	Glu	Val	Arg	Val
					100			105			110				

Ser	Glu	Leu	Gly	Leu	Gly	Tyr	Ala	Ser	Asp	Glu	Thr	Val	Leu	Phe	Arg
						115		120			125				

Tyr	Cys	Ala	Gly	Ala	Cys	Glu	Ala	Ala	Arg	Val	Tyr	Asp	Leu	Gly
						130		135			140			

Leu	Arg	Arg	Leu	Arg	Gln	Arg	Arg	Leu	Arg	Arg	Glu	Arg	Val	Arg
					145		150		155		160			

Ala Gln Pro Cys Cys Arg Pro Thr Ala Tyr Glu Asp Glu Val Ser Phe		
165	170	175
Leu Asp Ala His Ser Arg Tyr His Thr Val His Glu Leu Ser Ala Arg		
180	185	190
Glu Cys Ala Cys Val		
195		

## (2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 195 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Arg Arg Trp Lys Ala Ala Ala Leu Val Ser Leu Ile Cys Ser Ser			
1	5	10	15
Leu Leu Ser Val Trp Met Cys Gln Glu Gly Leu Leu Leu Gly His Arg			
20	25	30	
Leu Gly Pro Ala Leu Ala Pro Leu Arg Arg Pro Pro Arg Thr Leu Asp			
35	40	45	
Ala Arg Ile Ala Arg Leu Ala Gln Tyr Arg Ala Leu Leu Gln Gly Ala			
50	55	60	
Pro Asp Ala Val Glu Leu Arg Glu Leu Ser Pro Trp Ala Ala Arg Ile			
65	70	75	80
Pro Gly Pro Arg Arg Ala Gly Pro Arg Arg Arg Arg Ala Arg Pro			
85	90	95	
Gly Ala Arg Pro Cys Gly Leu Arg Glu Leu Glu Val Arg Val Ser Glu			
100	105	110	
Leu Gly Leu Gly Tyr Thr Ser Asp Glu Thr Val Leu Phe Arg Tyr Cys			
115	120	125	
Ala Gly Ala Cys Glu Ala Ala Ile Arg Ile Tyr Asp Leu Gly Leu Arg			
130	135	140	
Arg Leu Arg Gln Arg Arg Val Arg Arg Glu Arg Ala Arg Ala His			
145	150	155	160
Pro Cys Cys Arg Pro Thr Ala Tyr Glu Asp Glu Val Ser Phe Leu Asp			
165	170	175	
Val His Ser Arg Tyr His Thr Leu Gln Glu Leu Ser Ala Arg Glu Cys			
180	185	190	
Ala Cys Val			
195			

## (2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 306 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGCGGGTTGG	GGGCGCGGCC	TTGCAGGCTG	CGCGAGCTGG	AGGTGCGCGT	GAGCGAGCTG	60
GGCCTGGGCT	ACGCGTCCGA	CGAGACGGTG	CTGTTCCGCT	ACTGCGCAGG	CGCCTGCGAG	120
GCTGCCGCGC	GCGTCTACGA	CCTCGGGCTG	CGACGACTGC	GCCAGCGGCCG	GCGCCTGCGG	180
CGGGAGCGGG	TGCGCGCGCA	GCCCTGCTGC	CGCCCGACGG	CCTACGAGGA	CGAGGTGTCC	240
TTCCCTGGACG	CGCACAGCCG	CTACCACACG	GTGCACGAGC	TGTCGGCGCG	CGAGTGCGCC	300
TGGCGTG						306

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 300 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CCGGGGGGCTC	GGCCTTGTGG	GCTGCGCGAG	CTCGAGGTGC	GCGTGAGCGA	GCTGGGCCTG	60
GGCTACACGT	CGGATGAGAC	CGTGCTGTT	CGCTACTGCG	CAGGCGCGTG	CGAGGCGGCC	120
ATCCGCATCT	ACGACCTGGG	CCTCGGCCGC	CTGCGCCAGC	GGAGGCGCGT	GCGCAGAGAG	180
CGGGCGCGGG	CGCACCCGTG	TTGTCGCCCC	ACGGCCTATG	AGGACGAGGT	GTCCTTCCTG	240
GACGTGCACA	GCCGCTACCA	CACGCTGCAA	GAGCTGTCGG	CGCGGGAGTG	CGCGTGCCTG	300

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 594 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATGCAGCGCT	GGAAGGGCGGC	GGCCTTGGCC	TCAGTGCTCT	GCAGCTCCGT	GCTGTCCATC	60
TGGATGTGTC	GAGAGGGCCT	GCTTCTCAGC	CACCGCCTCG	GACCTGCGCT	GGTCCCCCTG	120
CACCGCCTGC	CTCGAACCCCT	GGACGCCCGG	ATTGCCGCC	TGGCCCAGTA	CCGTGCACTC	180

CTGCAGGGGG CCCCAGATGC GATGGAGCTG CGCGAGCTGA CGCCCTGGGC TGGGCGGCC	240
CCAGGTCCGC GCCGTCGGGC GGGGCCCCGG CGGCAGCGCG CGCGTGCAGCG GTTGGGGCG	300
CGGCCTTGCAG GGCTGCGCGA GCTGGAGGTG CGCGTGAGCG AGCTGGGCCT GGGCTACGCG	360
TCCGACGAGA CGGTGCTGTT CCGCTACTGC GCAGGCGCCT GCGAGGCTGC CGCGCGCGTC	420
TACGACCTCG GGCTGCGACG ACTGCGCCAG CGGCAGCGCC TGCGGCGGGA CGGGGTGCGC	480
GCGCAGCCCT GCTGCCGCC GACGGCCTAC GAGGACGAGG TGTCCCTCCT GGACGCGCAC	540
AGCCGCTACC ACACGGTGCA CGAGCTGTCG GCGCGCGAGT GCGCCTGCGT GTGA	594

## (2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 588 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ATGAGGCGCT GGAAGGCAGC GGCCCTGGTG TCGCTCATCT GCAGCTCCCT GCTATCTGTC	60
TGGATGTGCC AGGAGGGTCT GCTCTGGGC CACCGCCTGG GACCCGCGCT TGCCCCGCTA	120
CGACGCCCTC CACGCACCCCT GGACGCCCGC ATCGCCGCC TGGCCAGTA TCGCGCTCTG	180
CTCCAGGGCG CCCCGACGC GGTGGAGCTT CGAGAACATT CTCCCTGGGC TGCCCCGATC	240
CCGGGACCGC GCCGTCGAGC GGGTCCCCGG CGTCGGCGGG CGCGGCCGGG GGCTCGGCCT	300
TGTGGGCTGC GCGAGCTCGA GGTGCGCGTG AGCGAGCTGG GCCTGGGCTA CACGTGGAT	360
GAGACCGTGC TGTTCGGCTA CTGCGCAGGC GCGTGCAGG CGGCCATCCG CATCTACGAC	420
CTGGGCCTTC GGCGCCTGCG CCAGCGGAGG CGCGTGCAGCA GAGAGCGGGC GCGGGCGCAC	480
CCGTGTTGTC GCCCGACGGC CTATGAGGAC GAGGTGTCCCT TCCTGGACGT GCACAGCCGC	540
TACCACACGC TGCAAGAGCT GTCGGCGCGG GAGTGCAGCGT GCGTGTGA	588

## (2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 348 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GGAGGGAGAG CGCGCGGTGG TTTCGTCCGT GTGCCCGCG CCCGGCGCTC CTCGCGTGGC	60
CCCGCGTCCCT GAGCGCGCTC CAGCCTCCCA CGCGCGCCAC CCCGGGGTTC ACTGAGCCCG	120

GCGAGCCCGG GGAAGACAGA GAAAGAGAGG CCAGGGGGGG AACCCATGG CCCGGCCCGT	180
GTCCCGCACC CTGTGCGGTG GCCTCCTCCG GCACGGGGTC CCCGGTGC CTCGGTCCC	240
CGCGATCCGG ATGGCGCACG CAGTGGCTGG GGCCGGGCCG GGCTGGGTG GTCGGAGGAG	300
TCACCACTGA CGGGTCATC TGGAGCCCGT GGCAAGGCCGA GGCCCAGG	348

## (2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 87 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TGCTACCTCA CGCCCCCGA CCTGCGAAAG GGCCCTCCCT GCCGACCCCTC GCTGAGAACT	60
GAATTCACAT AAAGTGTGGG AACTCCC	87

## (2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Met Gln Arg Trp Lys Ala Ala Ala Leu Ala Ser Val Leu Cys Ser Ser	
1 5 10 15	
Val Leu Ser	

## (2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Met Arg Arg Trp Lys Ala Ala Ala Leu Val Ser Leu Ile Cys Ser Ser	
1 5 10 15	
Leu Leu Ser	

## (2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 57 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ATGCAGCGCT GGAAGGCGGC GGCCTTGGCC TCAGTGCTCT GCAGCTCCGT GCTGTCC

57

## (2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 57 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

ATGAGGCCGCT GGAAGGCAGC GGCCCTGGTG TCGCTCATCT GCAGCTCCCT GCTATCT

57

## (2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 76 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Ile Trp Met Cys Arg Glu Gly Leu Leu Leu Ser His Arg Leu Gly Pro  
 1 5 10 15

Ala Leu Val Pro Leu His Arg Leu Pro Arg Thr Leu Asp Ala Arg Ile  
 20 25 30

Ala Arg Leu Ala Gln Tyr Arg Ala Leu Leu Gln Gly Ala Pro Asp Ala  
 35 40 45

Met Glu Leu Arg Glu Leu Thr Pro Trp Ala Gly Arg Pro Pro Gly Pro  
 50 55 60

Arg Arg Arg Ala Gly Pro Arg Arg Arg Arg Ala Arg  
 65 70 75

## (2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 228 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

ATCTGGATGT GTCGAGAGGG CCTGCTTCTC AGCCACCGCC TCGGACCTGC GCTGGTCCCC	60
CTGCACCGCC TGCCTCGAAC CCTGGACGCC CGGATTGCC GCCTGGCCA GTACCGTGCA	120
CTCCTGCAGG GGGCCCCGGA TGCGATGGAG CTGCGCGAGC TGACGCCCTG GGCTGGCGG	180
CCCCCAGGTC CGCGCCGTCG GGCGGGGCC CGGCAGCGGT GCGCGCGT	228

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 228 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GTCTGGATGT GCCAGGAGGG TCTGCTCTTG GGCCACCGCC TGGGACCCGC GCTTGCCCCG	60
CTACGACGCC CTCCACGCAC CCTGGACGCC CGCATGCC GCCTGGCCA GTATCGCGCT	120
CTGCTCCAGG GCGCCCCCGA CGCGGTGGAG CTTCGAGAAC TTTCTCCCTG GGCTGCCCG	180
ATCCCAGGAC CGCGCCGTCG AGCGGGTCCC CGCGTCGGC GGGCGCGG	228

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 76 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Val Trp Met Cys Gln Glu Gly Leu Leu Leu Gly His Arg Leu Gly Pro	
1 5 10 15	
Ala Leu Ala Pro Leu Arg Arg Pro Pro Arg Thr Leu Asp Ala Arg Ile	
20 25 30	
Ala Arg Leu Ala Gln Tyr Arg Ala Leu Leu Gln Gly Ala Pro Asp Ala	
35 40 45	
Val Glu Leu Arg Glu Leu Ser Pro Trp Ala Ala Arg Ile Pro Gly Pro	
50 55 60	

Arg Arg Arg Ala Gly Pro Arg Arg Arg Arg Arg Ala Arg  
65 70 75

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 95 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

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Met Gln Arg Trp Lys Ala Ala Ala Leu Ala Ser Val Leu Cys Ser Ser
1 5 10 15

Val Leu Ser Ile Trp Met Cys Arg Glu Gly Leu Leu Leu Ser His Arg
20 25 30

Leu Gly Pro Ala Leu Val Pro Leu His Arg Leu Pro Arg Thr Leu Asp
35 40 45

Ala Arg Ile Ala Arg Leu Ala Gln Tyr Arg Ala Leu Leu Gln Gly Ala
50 55 60

Pro Asp Ala Met Glu Leu Arg Glu Leu Thr Pro Trp Ala Gly Arg Pro
65 70 75 80

Pro Gly Pro Arg Arg Arg Ala Gly Pro Arg Arg Arg Arg Ala Arg
85 90 95

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(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 95 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

## (2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 285 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

ATGCAGCGCT GGAAGGCGGC GGCCCTGGCC TCAGTGCTCT GCAGCTCCGT GCTGTCCATC	60
TGGATGTGTC GAGAGGGCCT GCTTCTCAGC CACCGCCTCG GACCTGCGCT GGTCCCCCTG	120
CACCGCCTGC CTCGAACCC CTGAGCGCCGG ATTGCCGCC TGGCCCAGTA CGGTGCACTC	180
CTGCAGGGGG CCCCCGGATGC GATGGAGCTG CGCGAGCTGA CGCCCTGGGC TGGGCGGCC	240
CCAGGTCCGC GCCGTCGGGC GGGGCCCCGG CGGCGGGCGCG CGCGT	285

## (2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 285 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

ATGAGGGCGCT GGAAGGCAGC GGCCCTGGTG TCGCTCATCT GCAGCTCCCT GCTATCTGTC	60
TGGATGTGCC AGGAGGGTCT GCTCTTGGGC CACCGCCTGG GACCCGCGCT TGCCCCGCTA	120
CGACGCCCTC CACGCACCC CTGAGCGCCGG ATCGCCGCC TGGCCCAGTA TCGCGCTCTG	180
CTCCAGGGCG CCCCCGACGC GGTGGAGCTT CGAGAACTTT CTCCCTGGGC TGCCCGCATC	240
CCGGGACCGC GCCGTCGAGC GGGTCCCCGG CGTCGGCGGG CGCGG	285

## (2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 169 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

ATGCAGCGCT GGAAGGCGGC GGCCCTGGCC TCAGTGCTCT GCAGCTCCGT GCTGTCCATC	60
TGGATGTGTC GAGAGGGCCT GCTTCTCAGC CACCGCCTCG GACCTGCGCT GGTCCCCCTG	120

CACCGCCTGC CTCGAACCCT GGACGCCCGG ATTGCCCGCC TGGCCCAGT

169

## (2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 425 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

ACCGTGCACT CCTGCAGGGG GCCCCGGATG CGATGGAGCT GCGCGAGCTG ACGCCCTGGG	60
CTGGGCGGCC CCCAGGTCCG CGCCGTCGGG CGGGGCCCCG GCGGCGGC GCAGCGTGC	120
GGTTGGGGGC GCGGCCTTGC GGGCTGCGCG AGCTGGAGGT GCGCGTGAGC GAGCTGGGCC	180
TGGGCTACGC GTCCGACGAG ACGGTGCTGT TCCGCTACTG CGCAGGCGCC TGCGAGGCTG	240
CCGCGCGCGT CTACGACCTC GGGCTGCGAC GACTGCGCCA GCGGCGGC CTGCGGCGGG	300
AGCGGGTGC CGCGCAGCCC TGCTGCCGCC CGACGGCCTA CGAGGACGAG GTGTCCTTCC	360
TGGACGCGCA CAGCCGCTAC CACACGGTGC ACGAGCTGTC GGCGCGCGAG TGCGCCTGCG	420
TGTGA	425

## (2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 169 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

ATGAGGCGCT GGAAGGCAGC GGCCCTGGTG TCGCTCATCT GCAGCTCCCT GCTATCTGTC	60
TGGATGTGCC AGGAGGGTCT GCTCTGGGC CACCGCCTGG GACCCGCGCT TGCCCCGCTA	120
CGACGCCCTC CACGCACCCCT GGACGCCCGC ATCGCCCGCC TGGCCCAAGT	169

## (2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 419 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

ATCGCGCTCT	GCTCCAGGGC	GCCCCGACG	CGGTGGAGCT	TCGAGAACTT	TCTCCCTGGG	60
CTGCCCGCAT	CCCGGGACCG	CGCCGTCGAG	CGGGTCCCCG	GCGTCGGCGG	GCGCGGCCGG	120
GGGCTCGGCC	TTGTGGGCTG	CGCGAGCTCG	AGGTGCGCGT	GAGCGAGCTG	GGCCTGGGCT	180
ACACGTCGGA	TGAGACCGTG	CTGTTCCGCT	ACTGCGCAGG	CGCGTGCAG	GCGGCCATCC	240
GCATCTACGA	CCTGGGCCCT	CGGCGCCTGC	GCCAGCGGAG	GCGCGTGCAG	AGAGAGCGGG	300
CGCGGGCGCA	CCCGTGTGT	CGCCCGACGG	CCTATGAGGA	CGAGGTGTCC	TTCCTGGACG	360
TGCACAGCCG	CTACCACACG	CTGCAAGAGC	TGTCGGCGCG	GGAGTGCGCG	TGCGTGTGA	419

## (2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 94 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Cys	Gly	Leu	Arg	Glu	Leu	Glu	Val	Arg	Val	Ser	Glu	Leu	Gly	Leu	Gly
1					5					10				15	
Tyr	Ala	Ser	Asp	Glu	Thr	Val	Leu	Phe	Arg	Tyr	Cys	Ala	Gly	Ala	Cys
					20				25				30		
Glu	Ala	Ala	Ala	Arg	Val	Tyr	Asp	Leu	Gly	Leu	Arg	Arg	Leu	Arg	Gln
					35				40				45		
Arg	Arg	Arg	Leu	Arg	Arg	Glu	Arg	Val	Arg	Ala	Gln	Pro	Cys	Cys	Arg
					50				55				60		
Pro	Thr	Ala	Tyr	Glu	Asp	Glu	Val	Ser	Phe	Leu	Asp	Ala	His	Ser	Arg
					65				70				75		80
Tyr	His	Thr	Val	His	Glu	Leu	Ser	Ala	Arg	Glu	Cys	Ala	Cys		
					85				90						

## (2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 94 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Cys	Gly	Leu	Arg	Glu	Leu	Glu	Val	Arg	Val	Ser	Glu	Leu	Gly	Leu	Gly
1					5					10				15	

Tyr Thr Ser Asp Glu Thr Val Leu Phe Arg Tyr Cys Ala Gly Ala Cys  
 20 25 30

Glu Ala Ala Ile Arg Ile Tyr Asp Leu Gly Leu Arg Arg Leu Arg Gln  
 35 40 45

Arg Arg Arg Val Arg Arg Glu Arg Ala Arg Ala His Pro Cys Cys Arg  
 50 55 60

Pro Thr Ala Tyr Glu Asp Glu Val Ser Phe Leu Asp Val His Ser Arg  
 65 70 75 80

Tyr His Thr Leu Gln Glu Leu Ser Ala Arg Glu Cys Ala Cys  
 85 90

## (2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 8 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
  - (A) NAME/KEY: Modified-site
  - (B) LOCATION: 2
  - (D) OTHER INFORMATION: /note= "SERINE OR THREONINE"

- (ix) FEATURE:
  - (A) NAME/KEY: Modified-site
  - (B) LOCATION: 3
  - (D) OTHER INFORMATION: /note= "GLUTAMIC ACID OR ASPARTIC ACID"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Val Xaa Xaa Leu Gly Leu Gly Tyr  
 1 5

## (2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 15 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
  - (A) NAME/KEY: Modified-site
  - (B) LOCATION: 2
  - (D) OTHER INFORMATION: /note= "THREONINE OR GLUTAMIC ACID"

- (ix) FEATURE:
  - (A) NAME/KEY: Modified-site
  - (B) LOCATION: 3
  - (D) OTHER INFORMATION: /note= "VALINE OR LEUCINE"

- (ix) FEATURE:
  - (A) NAME/KEY: Modified-site

(B) LOCATION: 4  
 (D) OTHER INFORMATION: /note= "LEUCINE OR ISOLEUCINE"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 9  
 (D) OTHER INFORMATION: /note= "ALANINE OR SERINE"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 11  
 (D) OTHER INFORMATION: /note= "ALANINE OR SERINE"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 13  
 (D) OTHER INFORMATION: /note= "GLUTAMIC ACID OR ASPARTIC  
 ACID"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 14  
 (D) OTHER INFORMATION: /note= "ALANINE OR SERINE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Glu	Xaa	Xaa	Xaa	Phe	Arg	Tyr	Cys	Xaa	Gly	Xaa	Cys	Xaa	Xaa	Ala
1														15

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 15 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 5  
 (D) OTHER INFORMATION: /note= "THREONINE OR VALINE OR  
 ISOLEUCINE"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 7  
 (D) OTHER INFORMATION: /note= "TYROSINE OR PHENYLALANINE"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 8  
 (D) OTHER INFORMATION: /note= "GLUTAMIC ACID OR ASPARTIC  
 ACID"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 10  
 (D) OTHER INFORMATION: /note= "GLUTAMIC ACID OR ASPARTIC  
 ACID"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site

(B) LOCATION: 11  
 (D) OTHER INFORMATION: /note= "VALINE OR LEUCINE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Cys	Cys	Arg	Pro	Xaa	Ala	Xaa	Xaa	Asp	Xaa	Xaa	Ser	Phe	Leu	Asp
1					5					10				15

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 11 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 5
- (D) OTHER INFORMATION: /note= "ALANINE OR SERINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 7
- (D) OTHER INFORMATION: /note= "ALANINE OR SERINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 9
- (D) OTHER INFORMATION: /note= "GLUTAMIC ACID OR ASPARTIC ACID"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 10
- (D) OTHER INFORMATION: /note= "SERINE OR ALANINE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Phe	Arg	Tyr	Cys	Xaa	Gly	Xaa	Cys	Xaa	Xaa	Ala
1					5				10	

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 11 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 5
- (D) OTHER INFORMATION: /note= "ALANINE OR SERINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 7

(D) OTHER INFORMATION: /note= "ALANINE OR SERINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 9

(D) OTHER INFORMATION: /note= "GLUTAMIC ACID OR ASPARTIC ACID"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 10

(D) OTHER INFORMATION: /note= "SERINE OR ALANINE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Phe	Arg	Tyr	Cys	Xaa	Gly	Xaa	Cys	Xaa	Xaa	Ala
1					5					10

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 5

(D) OTHER INFORMATION: /note= "ISOLEUCINE OR THREONINE OR VALINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 7

(D) OTHER INFORMATION: /note= "TYROSINE OR PHENYLALANINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 8

(D) OTHER INFORMATION: /note= "GLUTAMIC ACID OR ASPARTIC ACID"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 10

(D) OTHER INFORMATION: /note= "GLUTAMIC ACID OR ASPARTIC ACID"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Cys	Cys	Arg	Pro	Xaa	Ala	Xaa	Xaa	Asp	Xaa
1					5				10

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 2  
 (D) OTHER INFORMATION: /note= "TYROSINE OR PHENYLALANINE"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 3  
 (D) OTHER INFORMATION: /note= "GLUTAMIC ACID OR ASPARTIC ACID"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 5  
 (D) OTHER INFORMATION: /note= "GLUTAMIC ACID OR ASPARTIC ACID"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 6  
 (D) OTHER INFORMATION: /note= "VALINE OR LEUCINE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Ala	Xaa	Xaa	Asp	Xaa	Xaa	Ser	Phe	Leu	Asp
1				5				10	

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 8 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 2  
 (D) OTHER INFORMATION: /note= "GLUTAMIC ACID OR THREONINE"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 3  
 (D) OTHER INFORMATION: /note= "LEUCINE OR VALINE"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 4  
 (D) OTHER INFORMATION: /note= "ISOLEUCINE OR LEUCINE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Glu	Xaa	Xaa	Xaa	Phe	Arg	Tyr	Cys
1				5			

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 13 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 2  
 (D) OTHER INFORMATION: /note= "GLUTAMIC ACID OR THREONINE"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 3  
 (D) OTHER INFORMATION: /note= "LEUCINE OR VALINE"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 4  
 (D) OTHER INFORMATION: /note= "ISOLEUCINE OR LEUCINE"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 9  
 (D) OTHER INFORMATION: /note= "SERINE OR ALANINE"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 11  
 (D) OTHER INFORMATION: /note= "SERINE OR ALANINE"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 13  
 (D) OTHER INFORMATION: /note= "GLUTAMIC ACID OR ASPARTIC ACID"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Glu	Xaa	Xaa	Xaa	Phe	Arg	Tyr	Cys	Xaa	Gly	Xaa	Cys	Xaa
1					5						10	

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 23 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

GTNWSNGANY TNGGNYTNGG NTA

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 32 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

TTYMGNTAYT GYDSNGGNDS NTGYGANKCN GC

32

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 32 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GCNGMNTCRC ANSHNCCNSH RCARTANCKR AA

32

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

TCRTCNTRW ANGCNRYNGG NCKRCARCA

29

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

TCNARRAANS WNAVNTCRTC NTCRWANGC

29

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GARRMNBTNH TNTTYMGNTA YTG

23

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

GARRMNBTNH TNTTYMGNTA YTGYDSNGGN DSNTGHGA

38

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1023 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GGAGGGAGAG CGCGCGGTGG TTTCGTCCTG GTGCCCGCG CCCGGCGCTC CTCGCGTGGC	60
CCCGCGTCCT GAGCGCGCTC CAGCCTCCCA CGCGCGCCAC CCCGGGGTTTC ACTGAGCCCG	120
GCGAGCCCCG GGAAGACAGA GAAAGAGAGG CCAGGGGGGG AACCCCATGG CCCGGCCCCT	180
GTCCCGCACCC CTGTGCGGTG GCCTCCTCCG GCACGGGTC CCCGGGTCGC CTCCGGTCCC	240
CGCGATCCGG ATGGCGCACG CAGTGGCTGG GGCCGGGCCG GGCTCGGGTG GTCGGAGGAG	300
TCACCACTGA CCGGGTCATC TGGAGCCCGT GGCAGGCCGA GGCCCAGGAT GAGGCGCTGG	360
AAGGCAGCGG CCCTGGTGTG GCTCATCTGC AGCTCCCTGC TATCTGTCTG GATGTGCCAG	420
GAGGGTCTGC TCTTGGGCCA CCGCCTGGGA CCCGCGCTTG CCCCCTACG ACGCCCTCCA	480
CGCACCCCTGG ACGCCCCCAT CGCCCGCCTG GCCCAGTATC GCGCTCTGCT CCAGGGCGCC	540
CCCGACGCGG TGGAGCTTCG AGAACTTTCT CCCTGGCTG CCCGCATCCC GGGACCGCGC	600
CGTCGAGCGG GTCCCCGGCG TCGGCGGGCG CGGCCGGGGG CTCGGCCTTG TGGGCTGCGC	660
GAGCTCGAGG TGCGCGTGAG CGAGCTGGGC CTGGGCTACA CGTCGGATGA GACCGTGCTG	720
TTCCGCTACT GCGCAGGCAGC GTGCGAGGCG GCCATCCGCA TCTACGACCT GGGCCTTCGG	780

CGCCTGCGCC AGCGGAGGCG CGTGCAGA GAGCGGGCGC GGGCGCACCC GTGTTGTCGC	840
CCGACGGCCT ATGAGGACGA GGTGTCCTTC CTGGACGTGC ACAGCCGCTA CCACACGCTG	900
CAAGAGCTGT CGGCGCGGGA GTGCGCGTGC GTGTGATGCT ACCTCACGCC CCCCGACCTG	960
CGAAAGGGCC CTCCCTGCCG ACCCTCGCTG AGAACTGACT TCACATAAAG TGTGGAACT	1020
CCC	1023

## (2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

CCNACNGCNT AYGARGA	17
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## (2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 93 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Cys Val Leu Thr Ala Ile His Leu Asn Val Thr Asp Leu Gly Leu Gly	
1 5 10 15	
Tyr Glu Thr Lys Glu Glu Leu Ile Phe Arg Tyr Cys Ser Gly Ser Cys	
20 25 30	
Asp Ala Ala Glu Thr Thr Tyr Asp Lys Ile Leu Lys Asn Leu Ser Arg	
35 40 45	
Asn Arg Arg Leu Val Ser Asp Lys Val Gly Gln Ala Cys Cys Arg Pro	
50 55 60	
Ile Ala Phe Asp Asp Asp Leu Ser Phe Leu Asp Asp Asn Leu Val Tyr	
65 70 75 80	
His Ile Leu Arg Lys His Ser Ala Lys Arg Cys Gly Cys	
85 90	

## (2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

ARYTCYTGNA RNGTRTGRTA

20

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 28 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

GACGAGGTGT CCTTCCTGGA CGTACACACA

28

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

TAGCGGCTGT GTACGTCCAG GAAGGGACACC TCGT

34

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 26 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

CAGCGACGAC GCGTGCGCAA AGAGCG

26

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 47 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

TAYGARGACG AGGTGTCCTT CCTGGACGTA CACAGCCGCT AYCAYAC

47

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

GCGGCCATCC GCATCTACGA CCTGGG

26

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

CRTAGGCCGT CGGGCGRCAR CACGGGT

27

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

GCGCCGAAGG CCCAGGTCGT AGATGCG

27

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

CGCTACTGCG CAGGCAGCGTG CGARGCGGC 29

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

CGCCGACAGC TCTTGCAGCG TRTGGTA 27

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

GAGCTGGGCC TGGGCTACGC GTCCGACGAG 30

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

GCGACGCGTA CCATGAGGCG CTGGAAGGCA GCGGCCCTG 39

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

GACGGATCCG CATCACACGC ACGCGCACTC

30

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

GACCATATGC CGGGGGCTCG GCCTTGTGG

29

(2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

GACGGATCCG CATCACACGC ACGCGCACTC

30

(2) INFORMATION FOR SEQ ID NO:67:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 26 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

CAGCGACGAC GCGTGCGCAA AGAGCG

26

(2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

TAGCGGCTGT GTACGTCCAG GAAGGACACC TCGT

34

## (2) INFORMATION FOR SEQ ID NO:69:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

AAAAATCGGG GGTGYGTCTT A

21

## (2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

CATGCCTGGC CTACYTTGTC A

21

## (2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

CTGGCGTCCC AMCAAGGGTC TTTCG

24

## (2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

GCCAGTGGTG CCGTCGAGGC GGG

23

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

GGCCCAGGAT GAGGCCTGG AAGG

24

(2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

CCACTCCACT GCCTGAWATT CWACCCC

27

(2) INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

CCATGTGATT ATCGACCATT CGGC

24

(2) INFORMATION FOR SEQ ID NO:76:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 134 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Ser	Pro	Asp	Lys	Gln	Met	Ala	Val	Leu	Pro	Arg	Arg	Glu	Arg	Asn	Arg
1					5				10					15	

Gln Ala Ala Ala Ala Asn Pro Glu Asn Ser Arg Gly Lys Gly Arg Arg  
 20 25 30  
 Gly Gln Arg Gly Lys Asn Arg Gly Cys Val Leu Thr Ala Ile His Leu  
 35 40 45  
 Asn Val Thr Asp Leu Gly Leu Gly Tyr Glu Thr Lys Glu Glu Leu Ile  
 50 55 60  
 Phe Arg Tyr Cys Ser Gly Ser Cys Asp Ala Ala Glu Thr Thr Tyr Asp  
 65 70 75 80  
 Lys Ile Leu Lys Asn Leu Ser Arg Asn Arg Arg Leu Val Ser Asp Lys  
 85 90 95  
 Val Gly Gln Ala Cys Cys Arg Pro Ile Ala Phe Asp Asp Asp Leu Ser  
 100 105 110  
 Phe Leu Asp Asp Asn Leu Val Tyr His Ile Leu Arg Lys His Ser Ala  
 115 120 125  
 Lys Arg Cys Gly Cys Ile  
 130

## (2) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 134 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Ser Pro Asp Lys Gln Ala Ala Ala Leu Pro Arg Arg Glu Arg Asn Arg  
 1 5 10 15  
 Gln Ala Ala Ala Ala Ser Pro Glu Asn Ser Arg Gly Lys Gly Arg Arg  
 20 25 30  
 Gly Gln Arg Gly Lys Asn Arg Gly Cys Val Leu Thr Ala Ile His Leu  
 35 40 45  
 Asn Val Thr Asp Leu Gly Leu Gly Tyr Glu Thr Lys Glu Glu Leu Ile  
 50 55 60  
 Phe Arg Tyr Cys Ser Gly Ser Cys Glu Ser Ala Glu Thr Met Tyr Asp  
 65 70 75 80  
 Lys Ile Leu Lys Asn Leu Ser Arg Ser Arg Arg Leu Thr Ser Asp Lys  
 85 90 95  
 Val Gly Gln Ala Cys Cys Arg Pro Val Ala Phe Asp Asp Asp Leu Ser  
 100 105 110  
 Phe Leu Asp Asp Asn Leu Val Tyr His Ile Leu Arg Lys His Ser Ala  
 115 120 125  
 Lys Arg Cys Gly Cys Ile  
 130

## (2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 134 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Ser	Pro	Asp	Lys	Gln	Ala	Ala	Ala	Leu	Pro	Arg	Arg	Glu	Arg	Asn	Arg
1				5					10					15	
Gln Ala Ala Ala Ala Ser Pro Glu Asn Ser Arg Gly Lys Gly Arg Arg															
				20				25				30			
Gly Gln Arg Gly Lys Asn Arg Gly Cys Val Leu Thr Ala Ile His Leu															
				35				40				45			
Asn Val Thr Asp Leu Gly Leu Gly Tyr Glu Thr Lys Glu Glu Leu Ile															
				50				55				60			
Phe Arg Tyr Cys Ser Gly Ser Cys Glu Ala Ala Glu Thr Met Tyr Asp															
				65				70				75			80
Lys Ile Leu Lys Asn Leu Ser Arg Ser Arg Arg Leu Thr Ser Asp Lys															
				85				90				95			
Val Gly Gln Ala Cys Cys Arg Pro Val Ala Phe Asp Asp Asp Leu Ser															
				100				105				110			
Phe Leu Asp Asp Ser Leu Val Tyr His Ile Leu Arg Lys His Ser Ala															
				115				120				125			
Lys Arg Cys Gly Cys Ile															
				130											

## (2) INFORMATION FOR SEQ ID NO:79:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 89 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Cys	Arg	Leu	Trp	Ser	Leu	Thr	Leu	Pro	Val	Ala	Glu	Leu	Gly	Leu	Gly
1					5			10					15		
Tyr Ala Ser Glu Glu Lys Val Ile Phe Arg Tyr Cys Ala Gly Ser Cys															
				20			25				30				
Pro Gln Glu Ala Arg Thr Gln His Ser Leu Val Leu Ala Arg Leu Arg															
				35			40				45				

Gly Arg Gly Arg Ala His Gly Arg Pro Cys Cys Gln Pro Thr Ser Tyr  
 50 55 60  
 Ala Asp Val Thr Phe Leu Asp Asp Gln His His Trp Gln Gln Leu Pro  
 65 70 75 80  
 Gln Leu Ser Ala Ala Ala Cys Gly Cys  
 85

## (2) INFORMATION FOR SEQ ID NO:80:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 96 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

Ala Leu Ala Gly Ser Cys Arg Leu Trp Ser Leu Thr Leu Pro Val Ala  
 1 5 10 15  
 Glu Leu Gly Leu Gly Tyr Ala Ser Glu Glu Lys Val Ile Phe Arg Tyr  
 20 25 30  
 Cys Ala Gly Ser Cys Pro Gln Glu Ala Arg Thr Gln His Ser Leu Val  
 35 40 45  
 Leu Ala Arg Leu Arg Gly Arg Gly Arg Ala His Gly Arg Pro Cys Cys  
 50 55 60  
 Gln Pro Thr Ser Tyr Ala Asp Val Thr Phe Leu Asp Asp Gln His His  
 65 70 75 80  
 Trp Gln Gln Leu Pro Gln Leu Ser Ala Ala Ala Cys Gly Cys Gly Gly  
 85 90 95

## (2) INFORMATION FOR SEQ ID NO:81:

- (i) SEQUENCE CHARACTERISTICS:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

This sequence is intentionally skipped.

## (2) INFORMATION FOR SEQ ID NO:82:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 89 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

```

Cys Arg Leu Trp Ser Leu Thr Leu Pro Val Ala Glu Leu Gly Leu Gly
1 5 10 15

Tyr Ala Ser Glu Glu Lys Ile Ile Phe Arg Tyr Cys Ala Gly Ser Cys
20 25 30

Pro Gln Glu Val Arg Thr Gln His Ser Leu Val Leu Ala Arg Leu Arg
35 40 45

Gly Gln Gly Arg Ala His Gly Arg Pro Cys Cys Gln Pro Thr Ser Tyr
50 55 60

Ala Asp Val Thr Phe Leu Asp Asp His His His Trp Gln Gln Leu Pro
65 70 75 80

Gln Leu Ser Ala Ala Ala Cys Gly Cys
85

```

(2) INFORMATION FOR SEQ ID NO:83:

- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 91 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

```

Cys Arg Leu Trp Ser Leu Thr Leu Pro Val Ala Glu Leu Gly Leu Gly
1 5 10 15

Tyr Ala Ser Glu Glu Lys Ile Ile Phe Arg Tyr Cys Ala Gly Ser Cys
20 25 30

Pro Gln Glu Val Arg Thr Gln His Ser Leu Val Leu Ala Arg Leu Arg
35 40 45

Gly Gln Gly Arg Ala His Gly Arg Pro Cys Cys Gln Pro Thr Ser Tyr
50 55 60

Ala Asp Val Thr Phe Leu Asp Asp His His His Trp Gln Gln Leu Pro
65 70 75 80

Gln Leu Ser Ala Ala Ala Cys Gly Cys Gly Gly
85 90

```

(2) INFORMATION FOR SEQ ID NO:84:

- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 267 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

TGCCGACTGT GGAGCCTGAC CCTACCAGTG GCTGAGCTGG GCCTGGGCTA TGCCTCGGAG	60
GAGAAGGTCA TCTTCCGATA CTGTGCTGGC AGCTGTCCCC AAGAGGCCCG TACCCAGCAC	120
AGTCTGGTAC TGGCCCGGCT TCGAGGGCGG GGTCGAGCCC ATGGCCGACC CTGCTGCCAG	180
CCCACCAGCT ATGCTGATGT GACCTTCCTT GATGATCAGC ACCATTGGCA GCAGCTGCCT	240
CAGCTCTCAG CTGCAGCTTG TGGCTGT	267

## (2) INFORMATION FOR SEQ ID NO:85:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 267 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

TGCCGGCTGT GGAGCCTGAC CCTACCAGTG GCTGAGCTTG GCCTGGGCTA TGCCTCAGAG	60
GAGAAGATTA TCTTCCGATA CTGTGCTGGC AGCTGTCCCC AAGAGGTCCG TACCCAGCAC	120
AGTCTGGTGC TGGCCCGTCT TCGAGGGCAG GGTCGAGCTC ATGGCAGACC TTGCTGCCAG	180
CCCACCAGCT ATGCTGATGT GACCTTCCTT GATGACCACC ACCATTGGCA GCAGCTGCCT	240
CAGCTCTCAG CCGCAGCTTG TGGCTGT	267

## (2) INFORMATION FOR SEQ ID NO:86:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 273 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

TGCCGGCTGT GGAGCCTGAC CCTACCAGTG GCTGAGCTTG GCCTGGGCTA TGCCTCAGAG	60
GAGAAGATTA TCTTCCGATA CTGTGCTGGC AGCTGTCCCC AAGAGGTCCG TACCCAGCAC	120
AGTCTGGTGC TGGCCCGTCT TCGAGGGCAG GGTCGAGCTC ATGGCAGACC TTGCTGCCAG	180
CCCACCAGCT ATGCTGATGT GACCTTCCTT GATGACCACC ACCATTGGCA GCAGCTGCCT	240
CAGCTCTCAG CCGCAGCTTG TGGCTGTGGT GGC	273

## (2) INFORMATION FOR SEQ ID NO:87:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

Cys	Val	Leu	Thr	Ala	Ile	His	Leu	Asn	Val	Thr	Asp	Leu	Gly	Leu	Gly
1							5							10	
Tyr	Glu	Thr	Lys	Glu	Glu	Leu	Ile	Phe	Arg	Tyr	Cys	Ser	Gly	Ser	Cys
							20			25			30		
Glu	Ser	Ala	Glu	Thr	Met	Tyr	Asp	Lys	Ile	Leu	Lys	Asn	Leu	Ser	Arg
					35			40			45				
Ser	Arg	Arg	Leu	Thr	Ser	Asp	Lys	Val	Gly	Gln	Ala	Cys	Cys	Arg	Pro
					50			55			60				
Val	Ala	Phe	Asp	Asp	Asp	Leu	Ser	Phe	Leu	Asp	Asp	Asn	Leu	Val	Tyr
					65			70			75			80	
His	Ile	Leu	Arg	Lys	His	Ser	Ala	Lys	Arg	Cys	Gly	Cys	Ile		
					85			90							

(2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 95 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

Cys	Gly	Leu	Arg	Glu	Leu	Glu	Val	Arg	Val	Ser	Glu	Leu	Gly	Leu	Gly
1						5								10	
Tyr	Thr	Ser	Asp	Glu	Thr	Val	Leu	Phe	Arg	Tyr	Cys	Ala	Gly	Ala	Cys
						20			25			30			
Glu	Ala	Ala	Ile	Arg	Ile	Tyr	Asp	Leu	Gly	Leu	Arg	Arg	Leu	Arg	Gln
					35			40			45				
Arg	Arg	Arg	Val	Arg	Arg	Glu	Arg	Ala	Arg	Ala	His	Pro	Cys	Cys	Arg
					50			55			60				
Pro	Thr	Ala	Tyr	Glu	Asp	Glu	Val	Ser	Phe	Leu	Asp	Val	His	Ser	Arg
					65			70			75			80	
Tyr	His	Thr	Leu	Gln	Glu	Leu	Ser	Ala	Arg	Glu	Cys	Ala	Cys	Val	
					85			90			95				

(2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

Cys	Arg	Leu	Trp	Ser	Leu	Thr	Leu	Pro	Val	Ala	Glu	Leu	Gly	Leu	Gly
1				5											15
Tyr	Ala	Ser	Glu	Glu	Lys	Val	Ile	Phe	Arg	Tyr	Cys	Ala	Gly	Ser	Cys
			20					25							30
Pro	Gln	Glu	Ala	Arg	Thr	Gln	His	Ser	Leu	Val	Leu	Ala	Arg	Leu	Arg
	35					40								45	
Gly	Arg	Gly	Arg	Ala	His	Gly	Arg	Pro	Cys	Cys	Gln	Pro	Thr	Ser	Tyr
	50				55									60	
Ala	Asp	Val	Thr	Phe	Leu	Asp	Asp	Gln	His	His	Trp	Gln	Gln	Leu	Pro
	65				70				75						80
Gln	Leu	Ser	Ala	Ala	Ala	Cys	Gly	Cys	Gly	Gly					
					85				90						

(2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

TGCCTCAGAG GAGAAGATTA TC

22

(2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 7 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

Ala	Ser	Glu	Glu	Lys	Ile	Ile
1				5		

(2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

Leu Gly Leu Gly Tyr Glu Thr Lys Glu Glu Leu Ile Phe Arg Tyr Cys  
1               5                           10                           15

(2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

Leu Gly Leu Gly Tyr Thr Ser Asp Glu Thr Val Leu Phe Arg Tyr Cys  
1               5                           10                           15

(2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

Leu Gly Leu Gly Tyr Ala Ser Glu Glu Lys Ile Ile Phe Arg Tyr Cys  
1               5                           10                           15

(2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

AGTCGGGGTT GGGGTATGCC TCA 23

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

TATGCCTCAG AGGAGAAGAT TATCTT 26

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 336 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

CCTCAGAGGA GAAGATTATC TTCCGATACT GTGCTGGCAG CTGTCCCCAA GAGGTCCGTA	60
CCCAGCACAG TCTGGTGCTG GCCCGTCTTC GAGGGCAGGG TCGAGCTCAT GGCAGACCTT	120
GCTGCCAGCC CACCAGCTAT GCTGATGTGA CCTTCCTTGA TGACCACAC CATTGGCAGC	180
AGCTGCCTCA GCTCTCAGCC GCAGCTTGTG GCTGTGGTGG CTGAAGGCAG CCAGCCTGGT	240
CTCTCAGAAT CACAAGCAAG AGGCAGCCTT TGAAAGGCTC AGGTGACGTT ATTAGAAACT	300
TGCATAGGAG AAGATTAAGA AGAGAAAGGG GACCTG	336

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

Ala Cys Cys Arg Pro Val Ala Phe Asp Asp Asp Leu Ser Phe Leu Asp  
 1                   5                   10                   15

Asp

(2) INFORMATION FOR SEQ ID NO:99:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

Pro Cys Cys Arg Pro Thr Ala Tyr Glu Asp Glu Val Ser Phe Lys Asp  
 1                   5                   10                   15

Val

(2) INFORMATION FOR SEQ ID NO:100:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

Pro Cys Cys Gln Pro Thr Ser Tyr Ala Asp Val Thr Phe Leu Asp Asp  
 1                   5                   10                   15

(2) INFORMATION FOR SEQ ID NO:101:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 26 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

TCATCAAGGA AGGTCACATC AGCATA

26

(2) INFORMATION FOR SEQ ID NO:102:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

CCACCAACAGC CACAAGCTGC GGCTGAGAGC TG

32

(2) INFORMATION FOR SEQ ID NO:103:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 5 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

Ala Leu Ala Gly Ser  
1 5

(2) INFORMATION FOR SEQ ID NO:104:

- (i) SEQUENCE CHARACTERISTICS:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

This sequence is intentionally skipped

(2) INFORMATION FOR SEQ ID NO:105:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 544 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

GAGGGACCTG GACGCCCAT CAGGGTAAGA ATTCCCTGGGG GCCTCCCGAC TCCCCAATTC

60

CTTCTCTCAA AGCCCTCACT TTGCCTTACA ATCCTACTCT ACCTTGCACT AGGTAACAAAC

120

CATGTCCGTC TTCCAAGAGC CTTGGCTGGT TCATGCCGAC TGTGGAGCCT GACCCTACCA

180

GTGGCTGAGC TGGGCCTGGG CTATGCCTCG GAGGAGAAGG TCATCTTCCG ATACTGTGCT

240

GGCAGCTGTC	CCCAAGAGGC	CCGTACCCAG	CACAGTCTGG	TACTGGCCCG	GCTTCGAGGG	300
CGGGGTCGAG	CCCATGGCCG	ACCCTGCTGC	CAGCCCCACCA	GCTATGCTGA	TGTGACCTTC	360
CTTGATGATC	AGCACCATTG	GCAGCAGCTG	CCTCAGCTCT	CAGCTGCAGC	TTGTGGCTGT	420
GGTGGCTGAA	GGAGGCCAGT	CTGGTGTCTC	AGAATCACAA	GCATGAGACA	GGCTGGGCTT	480
TGAAAGGCTC	AGGTGACATT	ACTAGAAATT	TGCATAGGTA	AAGATAAGAA	GGGAAAGGAC	540
CAGG						544

(2) INFORMATION FOR SEQ ID NO:106:

- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 73 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

```

Ser Glu Glu Lys Ile Ile Phe Arg Tyr Cys Ala Gly Ser Cys Pro Gln
1           5           10          15

Glu Val Arg Thr Gln His Ser Leu Val Leu Ala Arg Leu Arg Gly Gln
20          25          30

Gly Arg Ala His Gly Arg Pro Cys Cys Gln Pro Thr Ser Tyr Ala Asp
35          40          45

Val Thr Phe Leu Asp Asp His His His Trp Gln Gln Leu Pro Gln Leu
50          55          60

```

(2) INFORMATION FOR SEQ ID NO:103:

- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 391 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - ii) MOLECULE TYPE: cDNA

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

```

TGCCGGCTGT GGAGCCTGAC CCTACCAGTG GCTGAGCTTG GCCTGGGCTA TGCCTCAGAG   60
GAGAAGAGATTA TCTTCCGATA CTGTGCTGGC AGCTGTCCCC AAGAGGTCCG TACCCAGCAC 120
AGTCTGGTGC TGGCCCGTCT TCGAGGGCAG GGTCGAGCTC ATGGCAGACC TTGCTGCCAG 180
CCCACCAAGCT ATGCTGATGT GACCTTCCTT GATGACCACC ACCATTGGCA GCAGCTGCCCT 240

```

CAGCTCTCAG CCGCAGCTTG TGGCTGTGGT GGCTGAAGGC GGCCAGCCTG GTCTCTCAGA	300
ATCACAAAGCA AGAGGCAGCC TTTGAAAGGC TCAGGTGACG TTATTAGAAA CTTGCATAGG	360
AGAAGATTAA GAAGAGAAAG GGGACCTGAT T	391

## (2) INFORMATION FOR SEQ ID NO:108:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 8 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /note= "SERINE, THREONINE, OR ALANINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /note= "GLUTAMIC ACID OR ASPARTIC ACID"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

```
Val Xaa Xaa Leu Gly Leu Gly Tyr
1           5
```

## (2) INFORMATION FOR SEQ ID NO:109:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 8 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 5
- (D) OTHER INFORMATION: /note= "ALANINE OR SERINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 7
- (D) OTHER INFORMATION: /note= "ALANINE OR SERINE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

```
Phe Arg Tyr Cys Xaa Gly Xaa Cys
1           5
```

## (2) INFORMATION FOR SEQ ID NO:110:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 8 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /note= "ASPARTIC ACID, GLUTAMIC ACID OR NO AMINO ACID"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /note= "VALINE OR LEUCINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 4
- (D) OTHER INFORMATION: /note= "SERINE OR THREONINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 8
- (D) OTHER INFORMATION: /note= "valine or aspartic acid"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

Asp	Xaa	Xaa	Xaa	Phe	Leu	Asp	Xaa
1				5			

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

Glu	Gly	Pro	Gly	Arg	Pro	Ile	Arg	Val	Arg	Ile	Pro	Gly	Gly	Leu	Pro
1				5				10						15	

Thr	Pro	Gln	Phe	Leu	Leu	Ser	Lys	Pro	Ser	Leu	Cys	Leu	Thr	Ile	Leu
				20				25					30		

Leu	Tyr	Leu	Ala	Leu	Gly	Asn	Asn	His	Val	Arg	Leu	Pro	Arg	Ala	Leu
				35				40				45			

Ala	Gly	Ser	Cys	Arg	Leu	Trp	Ser	Leu	Thr	Leu	Pro	Val	Ala	Glu	Leu
				50				55				60			

Gly	Leu	Gly	Tyr	Ala	Ser	Glu	Glu	Lys	Val	Ile	Phe	Arg	Tyr	Cys	Ala
65					70				75				80		

Gly	Ser	Cys	Pro	Gln	Glu	Ala	Arg	Thr	Gln	His	Ser	Leu	Val	Leu	Ala
				85				90				95			

Arg Leu Arg Gly Arg Gly Arg Ala His Gly Arg Pro Cys Cys Gln Pro  
 100 105 110

Thr Ser Tyr Ala Asp Val Thr Phe Leu Asp Asp Gln His His Trp Gln  
 115 120 125

Gln Leu Pro Gln Leu Ser Ala Ala Ala Cys Gly Cys Gly Gly  
 130 135 140

(2) INFORMATION FOR SEQ ID NO:112:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 5 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

Ala Leu Pro Gly Leu  
 1 5

(2) INFORMATION FOR SEQ ID NO:113:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 12 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /note= "THREONINE, GLUTAMIC ACID OR LYSINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /note= "VALINE, LEUCINE OR ISOLEUCINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 4
- (D) OTHER INFORMATION: /note= "LEUCINE OR ISOLEUCINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 9
- (D) OTHER INFORMATION: /note= "ALANINE OR SERINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 11
- (D) OTHER INFORMATION: /note= "ALANINE OR SERINE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

Glu Xaa Xaa Xaa Phe Arg Tyr Cys Xaa Gly Xaa Cys  
1                   5                           10

(2) INFORMATION FOR SEQ ID NO:114:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 16 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /note= "ARGININE OR GLUTAMINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 5
- (D) OTHER INFORMATION: /note= "THREONINE, VALINE OR ISOLEUCINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 6
- (D) OTHER INFORMATION: /note= "ALANINE OR SERINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 7
- (D) OTHER INFORMATION: /note= "TYROSINE OR PHENYLALANINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 8
- (D) OTHER INFORMATION: /note= "GLUTAMIC ACID, ASPARTIC ACID OR ALANINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 10
- (D) OTHER INFORMATION: /note= "GLUTAMIC ACID, ASPARTIC ACID OR NO AMINO ACID"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 11
- (D) OTHER INFORMATION: /note= "VALINE OR LEUCINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 12
- (D) OTHER INFORMATION: /note= "SERINE OR THREONINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 16
- (D) OTHER INFORMATION: /note= "ASPARTIC ACID OR VALINE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

Cys Cys Xaa Pro Xaa Xaa Xaa Xaa Asp Xaa Xaa Xaa Phe Leu Asp Xaa  
 1                   5                   10                   15

(2) INFORMATION FOR SEQ ID NO:115:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

GTNDGNGANY TGGGNYTGGG NTA

23

(2) INFORMATION FOR SEQ ID NO:116:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

GANBTNWCNT TYYTNGANG

19

(2) INFORMATION FOR SEQ ID NO:117:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

GANBTNWCNT TYYTNGANGW

20

(2) INFORMATION FOR SEQ ID NO:118:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:  
 TTYMGNAYT GYDSNGGNDS NTG 23
- (2) INFORMATION FOR SEQ ID NO:119:
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 20 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:  
 GTNDGNGANY TGGGNYTNGG 20
- (2) INFORMATION FOR SEQ ID NO:120:
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 23 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:  
 GTNDGNGANY TGGGNYTGGG NTT 23
- (2) INFORMATION FOR SEQ ID NO:121:
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 20 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:  
 WCNTCNARRA ANGWNNAVNTC 20
- (2) INFORMATION FOR SEQ ID NO:122:
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 19 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

WCNTCNARRA ANGWNNAVNT

19

(2) INFORMATION FOR SEQ ID NO:123:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

CANSHNCCNS HRCARTANCK RAA

23

(2) INFORMATION FOR SEQ ID NO:124:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

CANSHNCCNS HRCARTANCK RAANA

25

(2) INFORMATION FOR SEQ ID NO:125:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 8 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /note= "THREONINE, SERINE OR ALANINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /note= "GLUTAMIC ACID OR ASPARTIC ACID"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

Val Xaa Xaa Leu Gly Leu Gly Tyr  
1 5

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /note= "ASPARTIC ACID OR GLUTAMIC ACID"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /note= "VALINE OR LEUCINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /note= "THREONINE OR SERINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 6
- (D) OTHER INFORMATION: /note= "ASPARTIC ACID OR GLUTAMIC ACID"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 7
- (D) OTHER INFORMATION: /note= "ASPARTIC ACID OR VALINE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

Xaa Xaa Xaa Phe Leu Xaa Xaa  
1 5

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 5
- (D) OTHER INFORMATION: /note= "SERINE OR ALANINE"

(ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 7  
(D) OTHER INFORMATION: /note= "SERINE OR ALANINE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

Phe Arg Tyr Cys Xaa Gly Xaa Cys  
1 5

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 7 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 2  
(D) OTHER INFORMATION: /note= "THREONINE, SERINE OR  
ALANINE"

(ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 3  
(D) OTHER INFORMATION: /note= "ASPARTIC ACID OR GLUTAMIC  
ACID"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

Val Xaa Xaa Leu Gly Leu Gly  
1 5

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 8 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 2  
(D) OTHER INFORMATION: /note= "THREONINE, SERINE OR  
ALANINE"

(ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 3  
(D) OTHER INFORMATION: /note= "GLUTAMIC ACID OR ASPARTIC  
ACID"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

Val Xaa Xaa Leu Gly Leu Gly Phe  
 1 5

## (2) INFORMATION FOR SEQ ID NO:130:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 9 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (ix) FEATURE:
  - (A) NAME/KEY: Modified-site
  - (B) LOCATION: 1
  - (D) OTHER INFORMATION: /note= "ISOLEUCINE OR LEUCINE"
- (ix) FEATURE:
  - (A) NAME/KEY: Modified-site
  - (B) LOCATION: 6
  - (D) OTHER INFORMATION: /note= "SERINE OR ALANINE"
- (ix) FEATURE:
  - (A) NAME/KEY: Modified-site
  - (B) LOCATION: 8
  - (D) OTHER INFORMATION: /note= "SERINE OR ALANINE"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

Xaa Phe Arg Tyr Cys Xaa Gly Xaa Cys  
 1 5

## (2) INFORMATION FOR SEQ ID NO:131:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 559 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

ATGGCTGCAG GAAGACTTCG GATCCTGTGT CTGCTGCTCC TGTCCCTGCA CCCGAGCCTC	60
GGCTGGGTCC TTGATCTTCA AGAGGCTTCT GTGGCAGATA AGCTCTCATT TGGGAAGATG	120
GCAGAGACTA GAGGGACCTG GACGCCCAT CAGGGTAAGA ATTCCCTGGGG GCCTCCCGAC	180
TCCCCAATTC CTTCTCTCAA AGCCCTCACT TTGCCTTACA ATCCTACTCT ACCTTGCACT	240
AGGTAACAAAC CATGTCCGTC TTCCAAGAGC CTTGGCTGGT TCATGCCGAC TGTGGAGCCT	300
GACCCTACCA GTGGCTGAGC TGGGCCTGGG CTATGCCTCG GAGGAGAAGG TCATCTTCCG	360
ATACTGTGCT GGCAGCTGTC CCCAAGAGGC CCGTACCCAG CACAGTCTGG TACTGGCCCG	420
GCTTCGAGGG CGGGGTCGAG CCCATGGCCG ACCCTGCTGC CAGCCCACCA GCTATGCTGA	480

TGTGACCTTC CTTGATGATC AGCACCAATTG GCAGCAGCTG CCTCAGCTCT CAGCTGCAGC	540
TTGTGGCTGT GGTGGCTGA	559

## (2) INFORMATION FOR SEQ ID NO:132:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 133 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

```

Pro Asp Ala Arg Gly Val Pro Val Ala Asp Gly Glu Phe Ser Ser Glu
1           5           10          15

Gln Val Ala Lys Ala Gly Gly Thr Trp Leu Gly Thr His Arg Pro Leu
20          25          30          35          40          45

Ala Arg Leu Arg Arg Ala Leu Ser Gly Pro Cys Gln Leu Trp Ser Leu
35          40          45          50          55          60

Thr Leu Ser Val Ala Glu Leu Gly Leu Gly Tyr Ala Ser Glu Glu Lys
50          55          60          65          70          75          80

Val Ile Phe Arg Tyr Cys Ala Gly Ser Cys Pro Arg Gly Ala Arg Thr
65          70          75          80          85          90          95

Gln His Gly Leu Ala Leu Ala Arg Leu Gln Gly Gln Gly Arg Ala His
85          90          95          100         105         110

Gly Gly Pro Cys Cys Arg Pro Thr Arg Tyr Thr Asp Val Ala Phe Leu
100         105         110         115         120         125

Asp Asp Arg His Arg Trp Gln Arg Leu Pro Gln Leu Ser Ala Ala Ala
115         120         125         130

```

Cys Gly Cys Gly Gly

## (2) INFORMATION FOR SEQ ID NO:133:

- (i) SEQUENCE CHARACTERISTICS:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

This sequence is intentionally skipped

## (2) INFORMATION FOR SEQ ID NO:134:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 93 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

Cys	Val	Leu	Thr	Ala	Ile	His	Leu	Asn	Val	Thr	Asp	Leu	Gly	Leu	Gly
1					5					10				15	
Tyr	Glu	Thr	Lys	Glu	Glu	Leu	Ile	Phe	Arg	Tyr	Cys	Ser	Gly	Ser	Cys
				20				25				30			
Glu	Ala	Ala	Glu	Thr	Met	Tyr	Asp	Lys	Ile	Leu	Lys	Asn	Leu	Ser	Arg
				35			40				45				
Ser	Arg	Arg	Leu	Thr	Ser	Asp	Lys	Val	Gly	Gln	Ala	Cys	Cys	Arg	Pro
				50			55				60				
Val	Ala	Phe	Asp	Asp	Asp	Leu	Ser	Phe	Leu	Asp	Asp	Ser	Leu	Val	Tyr
				65		70			75				80		
His	Ile	Leu	Arg	Lys	His	Ser	Ala	Lys	Arg	Cys	Gly	Cys			
				85			90								

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

Met	Ala	Ala	Gly	Arg	Leu	Arg	Ile	Leu	Cys	Leu	Leu	Leu	Leu	Ser	Leu
1					5					10				15	
His	Pro	Ser	Leu	Gly	Trp	Val									
				20											

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

Met	Ala	Ala	Gly	Arg	Leu	Arg	Ile	Leu	Phe	Leu	Leu	Leu	Leu	Ser	Leu
1					5					10				15	
His	Leu	Gly	Leu	Gly	Trp	Val									
				20											

(2) INFORMATION FOR SEQ ID NO:137:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 23 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

AATCCCCAGG ACAGGCAGGG AAT

23

(2) INFORMATION FOR SEQ ID NO:138:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 35 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

CGGTACCCAG ATCTTCAGCC ACCACAGCCA CAAGC

35

(2) INFORMATION FOR SEQ ID NO:139:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 76 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

GGACTATCAT ATGGCCCACC ACCACCACCA CCACCACAC GACGACGACG ACAAGGCCTT

60

GGCTGGTTCA TGCCGA

76

(2) INFORMATION FOR SEQ ID NO:140:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 32 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

TGCTGTCACC ATGGCTGCAG GAAGACTTCG GA

32

## (2) INFORMATION FOR SEQ ID NO:141:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 96 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

Ala	Leu	Ala	Gly	Ser	Cys	Arg	Leu	Trp	Ser	Leu	Thr	Leu	Pro	Val	Ala
1															15

Glu	Leu	Gly	Leu	Gly	Tyr	Ala	Ser	Glu	Glu	Lys	Val	Ile	Phe	Arg	Tyr
															30
20															

Cys	Ala	Gly	Ser	Cys	Pro	Gln	Glu	Ala	Arg	Thr	Gln	His	Ser	Leu	Val
															45
35															

Leu	Ala	Arg	Leu	Arg	Gly	Arg	Ala	His	Gly	Arg	Pro	Cys	Cys	
50														

Arg	Pro	Thr	Ala	Tyr	Glu	Asp	Glu	Val	Ser	Phe	Leu	Asp	Val	His	Ser
															80
65															

Arg	Tyr	His	Thr	Leu	Gln	Glu	Leu	Ser	Ala	Arg	Glu	Cys	Ala	Cys	Val
															95
85															

## (2) INFORMATION FOR SEQ ID NO:142:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 23 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

TAATACGACT CACTATAGGG GAA

23

## (2) INFORMATION FOR SEQ ID NO:143:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 49 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

TCGTCTTCGT AAGCAGTCGG ACGGCAGCAG GGTGGGCCAT GGGCTCGAC

49

(2) INFORMATION FOR SEQ ID NO:144:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

TGCTGCCGTC CGACTGCTTA CGAAGACGA

29

(2) INFORMATION FOR SEQ ID NO:145:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

GTTATGCTAG TTATTGCTCA GCGGT

25

(2) INFORMATION FOR SEQ ID NO:146:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 100 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

Pro	Gly	Ala	Arg	Pro	Cys	Gly	Leu	Arg	Glu	Leu	Glu	Val	Arg	Val	Ser
1					5				10				15		

Glu	Leu	Gly	Leu	Gly	Tyr	Thr	Ser	Asp	Glu	Thr	Val	Leu	Phe	Arg	Tyr
					20			25					30		

Cys	Ala	Gly	Ala	Cys	Glu	Ala	Ala	Ile	Arg	Ile	Tyr	Asp	Leu	Gly	Leu
					35			40			45				

Arg	Arg	Leu	Arg	Gln	Arg	Arg	Val	Arg	Arg	Glu	Arg	Ala	Arg	Ala
					50			55		60				

His	Pro	Cys	Cys	Gln	Pro	Thr	Ser	Tyr	Ala	Asp	Val	Thr	Phe	Leu	Asp
65					70				75					80	
Asp	Gln	His	His	Trp	Gln	Gln	Leu	Pro	Gln	Leu	Ser	Ala	Ala	Ala	Cys
				85					90					95	
Gly	Cys	Gly	Gly												
				100											

## (2) INFORMATION FOR SEQ ID NO:147:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 50 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

CACATCAGCA TAGCTGGTGG GCTGGCAGCA CGGGTGAGCA CGAGCACGTT 50

## (2) INFORMATION FOR SEQ ID NO:148:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

TGCTGCCAGC CCACCAGCTA TGCTG 25

## (2) INFORMATION FOR SEQ ID NO:149:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

CCTCGGAGGA GAAGGTCATC TTC 23

## (2) INFORMATION FOR SEQ ID NO:150:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 98 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

Cys	Cys	Val	Arg	Gln	Leu	Tyr	Ile	Asp	Phe	Arg	Lys	Asp	Leu	Gly	Trp
1				5					10		15				
Lys	Trp	Ile	His	Glu	Pro	Lys	Gly	Tyr	His	Ala	Asn	Phe	Cys	Leu	Gly
	20					25						30			
Pro	Cys	Pro	Tyr	Ile	Trp	Ser	Leu	Asp	Thr	Gln	Tyr	Ser	Lys	Val	Leu
		35					40			45					
Ala	Leu	Tyr	Asn	Gln	His	Asn	Pro	Gly	Ala	Ser	Ala	Ala	Pro	Cys	Cys
		50				55				60					
Val	Pro	Gln	Ala	Leu	Glu	Pro	Leu	Pro	Ile	Val	Tyr	Tyr	Val	Gly	Arg
	65				70				75			80			
Lys	Pro	Lys	Val	Glu	Gln	Leu	Ser	Asn	Met	Ile	Val	Arg	Ser	Cys	Lys
		85					90				95				
Cys	Ser														

(2) INFORMATION FOR SEQ ID NO:151:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 98 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

Cys	Cys	Leu	Arg	Pro	Leu	Tyr	Ile	Asp	Phe	Lys	Arg	Asp	Leu	Gly	Trp
1				5					10		15				
Lys	Trp	Ile	His	Glu	Pro	Lys	Gly	Tyr	Asn	Ala	Asn	Phe	Cys	Ala	Gly
	20					25					30				
Ala	Cys	Pro	Tyr	Leu	Trp	Ser	Ser	Asp	Thr	Gln	His	Ser	Arg	Val	Leu
		35					40			45					
Ser	Leu	Tyr	Asn	Thr	Ile	Asn	Pro	Glu	Ala	Ser	Ala	Ser	Pro	Cys	Cys
		50				55				60					
Val	Ser	Gln	Asp	Leu	Glu	Pro	Leu	Thr	Ile	Leu	Tyr	Tyr	Ile	Gly	Lys
	65				70				75			80			
Thr	Pro	Lys	Ile	Glu	Gln	Leu	Ser	Asn	Met	Ile	Val	Lys	Ser	Cys	Lys
		85					90				95				
Cys	Ser														

## (2) INFORMATION FOR SEQ ID NO:152:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 98 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

Cys	Cys	Val	Arg	Pro	Leu	Tyr	Ile	Asp	Phe	Arg	Gln	Asp	Leu	Gly	Trp
1					5					10					15
Lys	Trp	Val	His	Glu	Pro	Lys	Gly	Tyr	Tyr	Ala	Asn	Phe	Cys	Ser	Gly
					20				25					30	
Pro	Cys	Pro	Tyr	Leu	Arg	Ser	Ala	Asp	Thr	Thr	His	Ser	Thr	Val	Leu
					35				40					45	
Gly	Leu	Tyr	Asn	Thr	Leu	Asn	Pro	Glu	Ala	Ser	Ala	Ser	Pro	Cys	Cys
					50			55				60			
Val	Pro	Gln	Asp	Leu	Glu	Pro	Leu	Thr	Ile	Leu	Tyr	Tyr	Val	Gly	Arg
					65			70			75			80	
Thr	Pro	Lys	Val	Glu	Gln	Leu	Ser	Asn	Met	Val	Val	Lys	Ser	Cys	Lys
					85					90				95	
Cys	Ser														

## (2) INFORMATION FOR SEQ ID NO:153:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 106 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

Cys	Cys	Lys	Lys	Gln	Phe	Phe	Val	Ser	Phe	Lys	Asp	Ile	Gly	Trp	Asn
1								5		10					15
Asp	Trp	Ile	Ile	Ala	Pro	Ser	Gly	Tyr	His	Ala	Asn	Tyr	Cys	Glu	Gly
					20			25						30	
Glu	Cys	Pro	Ser	His	Ile	Ala	Gly	Thr	Ser	Gly	Ser	Ser	Leu	Ser	Phe
					35			40					45		
His	Ser	Thr	Val	Ile	Asn	His	Tyr	Arg	Met	Arg	Gly	His	Ser	Pro	Phe
					50			55			60				
Ala	Asn	Leu	Lys	Ser	Cys	Cys	Val	Pro	Thr	Lys	Leu	Arg	Pro	Met	Ser
					65			70			75			80	

Met Leu Tyr Tyr Asp Asp Gly Gln Asn Ile Ile Lys Lys Asp Ile Gln  
 85 90 95

Asn Met Ile Val Glu Glu Cys Gly Cys Ser  
 100 105

(2) INFORMATION FOR SEQ ID NO:154:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 105 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

Cys Cys Arg Gln Gln Phe Phe Ile Asp Phe Arg Leu Ile Gly Trp Asn  
 1 5 10 15

Asp Trp Ile Ile Ala Pro Thr Gly Tyr Tyr Gly Asn Tyr Cys Glu Gly  
 20 25 30

Ser Cys Pro Ala Tyr Leu Ala Gly Val Pro Gly Ser Ala Ser Ser Phe  
 35 40 45

His Thr Ala Val Val Asn Gln Tyr Arg Met Arg Gly Leu Asn Pro Gly  
 50 55 60

Thr Val Asn Ser Cys Cys Ile Pro Thr Lys Leu Ser Thr Met Ser Met  
 65 70 75 80

Leu Tyr Phe Asp Asp Glu Tyr Asn Ile Val Lys Arg Asp Val Pro Asn  
 85 90 95

Met Ile Val Glu Glu Cys Gly Cys Ala  
 100 105

(2) INFORMATION FOR SEQ ID NO:155:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 101 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

Cys Arg Arg Val Lys Phe Gln Val Asp Phe Asn Leu Ile Gly Trp Gly  
 1 5 10 15

Ser Trp Ile Ile Tyr Pro Lys Gln Tyr Asn Ala Tyr Arg Cys Glu Gly  
 20 25 30

Glu Cys Pro Asn Pro Val Gly Glu Glu Phe His Pro Thr Asn His Ala  
 35 40 45

Tyr Ile Gln Ser Leu Leu Lys Arg Tyr Gln Pro His Arg Val Pro Ser  
 50 55 60

Thr Cys Cys Ala Pro Val Lys Thr Lys Pro Leu Ser Met Leu Tyr Val  
 65 70 75 80

Asp Asn Gly Arg Val Leu Leu Glu His His Lys Asp Met Ile Val Glu  
 85 90 95

Glu Cys Gly Cys Leu  
 100

## (2) INFORMATION FOR SEQ ID NO:156:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 101 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

Cys Lys Arg His Pro Leu Tyr Val Asp Phe Ser Asp Val Gly Trp Asn  
 1 5 10 15

Asp Trp Ile Val Ala Pro Pro Gly Tyr His Ala Phe Tyr Cys His Gly  
 20 25 30

Glu Cys Pro Phe Pro Leu Ala Asp His Leu Asn Ser Thr Asn His Ala  
 35 40 45

Ile Val Gln Thr Leu Val Asn Ser Val Asn Ser Lys Ile Pro Lys Ala  
 50 55 60

Cys Cys Val Pro Thr Glu Leu Ser Ala Ile Ser Met Leu Tyr Leu Asp  
 65 70 75 80

Glu Asn Glu Lys Val Val Leu Lys Asn Tyr Gln Asp Met Val Val Glu  
 85 90 95

Gly Cys Gly Cys Arg  
 100

## (2) INFORMATION FOR SEQ ID NO:157:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 101 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

Cys Arg Arg His Ser Leu Tyr Val Asp Phe Ser Asp Val Gly Trp Asn  
 1 5 10 15

Asp Trp Ile Val Ala Pro Pro Gly Tyr Gln Ala Phe Tyr Cys His Gly  
 20 25 30

Asp Cys Pro Phe Pro Leu Ala Asp His Leu Asn Ser Thr Asn His Ala  
 35 40 45

Ile Val Gln Thr Leu Val Asn Ser Val Asn Ser Ser Ile Pro Lys Ala  
 50 55 60

Cys Cys Val Pro Thr Glu Leu Ser Ala Ile Ser Met Leu Tyr Leu Asp  
 65 70 75 80

Glu Tyr Asp Lys Val Val Leu Lys Asn Tyr Gln Glu Met Val Val Glu  
 85 90 95

Gly Cys Gly Cys Arg  
 100

## (2) INFORMATION FOR SEQ ID NO:158:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 102 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

Cys Arg Arg His Ser Leu Tyr Val Asp Phe Ser Asp Val Gly Trp Asp  
 1 5 10 15

Asp Trp Ile Val Ala Pro Leu Gly Tyr Asp Ala Tyr Tyr Cys His Gly  
 20 25 30

Lys Cys Pro Phe Pro Leu Ala Asp His Phe Asn Ser Thr Asn His Ala  
 35 40 45

Val Val Gln Thr Leu Val Asn Asn Met Asn Pro Gly Lys Val Pro Lys  
 50 55 60

Ala Cys Cys Val Pro Thr Gln Leu Asp Ser Val Ala Met Leu Tyr Leu  
 65 70 75 80

Asn Asp Gln Ser Thr Val Val Leu Lys Asn Tyr Gln Glu Met Thr Val  
 85 90 95

Val Gly Cys Gly Cys Arg  
 100

## (2) INFORMATION FOR SEQ ID NO:159:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 102 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

Cys Lys Lys His Glu Leu Tyr Val Ser Phe Arg Asp Leu Gly Trp Gln  
 1                   5   10                   15  
 Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala Ala Phe Tyr Cys Asp Gly  
 20                   25   30  
 Glu Cys Ser Phe Pro Leu Asn Ala His Met Asn Ala Thr Asn His Ala  
 35                   40   45  
 Ile Val Gln Thr Leu Val His Leu Met Phe Pro Asp His Val Pro Lys  
 50                   55   60  
 Pro Cys Cys Ala Pro Thr Lys Leu Asn Ala Ile Ser Val Leu Tyr Phe  
 65                   70   75                   80  
 Asp Asp Ser Ser Asn Val Ile Leu Lys Lys Tyr Arg Asn Met Val Val  
 85                   90   95  
 Arg Ser Cys Gly Cys His  
 100

## (2) INFORMATION FOR SEQ ID NO:160:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 102 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

Cys Arg Lys His Glu Leu Tyr Val Ser Phe Gln Asp Leu Gly Trp Gln  
 1                   5   10                   15  
 Asp Trp Ile Ile Ala Pro Lys Gly Tyr Ala Ala Asn Tyr Cys Asp Gly  
 20                   25   30  
 Glu Cys Ser Phe Pro Leu Asn Ala His Met Asn Ala Thr Asn His Ala  
 35                   40   45  
 Ile Val Gln Thr Leu Val His Leu Met Asn Pro Glu Tyr Val Pro Lys  
 50                   55   60  
 Pro Cys Cys Ala Pro Thr Lys Leu Asn Ala Ile Ser Val Leu Tyr Phe  
 65                   70   75                   80  
 Asp Asp Asn Ser Asn Val Ile Leu Lys Lys Tyr Arg Asn Met Val Val  
 85                   90   95  
 Arg Ala Cys Gly Cys His  
 100

## (2) INFORMATION FOR SEQ ID NO:161:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 102 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

Cys	Lys	Lys	His	Glu	Leu	Tyr	Val	Ser	Phe	Arg	Asp	Leu	Gly	Trp	Gln
1				5				10						15	
Asp	Trp	Ile	Ile	Ala	Pro	Glu	Gly	Tyr	Ala	Ala	Tyr	Tyr	Cys	Glu	Gly
	20							25					30		
Glu	Cys	Ala	Phe	Pro	Leu	Asn	Ser	Tyr	Met	Asn	Ala	Thr	Asn	His	Ala
	35					40			45						
Ile	Val	Gln	Thr	Leu	Val	His	Phe	Ile	Asn	Pro	Glu	Thr	Val	Pro	Lys
	50					55			60						
Pro	Cys	Cys	Ala	Pro	Thr	Gln	Leu	Asn	Ala	Ile	Ser	Val	Leu	Tyr	Phe
	65				70			75					80		
Asp	Asp	Ser	Ser	Asn	Val	Ile	Leu	Lys	Lys	Tyr	Arg	Asn	Met	Val	Val
	85					90				95					
Arg	Ala	Cys	Gly	Cys	His										
	100														

(2) INFORMATION FOR SEQ ID NO:162:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 102 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

Cys	Arg	Arg	His	Glu	Leu	Tyr	Val	Ser	Phe	Gln	Asp	Leu	Gly	Trp	Leu
1				5				10						15	
Asp	Trp	Val	Ile	Ala	Pro	Gln	Gly	Tyr	Ser	Ala	Tyr	Tyr	Cys	Glu	Gly
	20					25			30						
Glu	Cys	Ser	Phe	Pro	Leu	Asp	Ser	Cys	Met	Asn	Ala	Thr	Asn	His	Ala
	35					40			45						
Ile	Leu	Gln	Ser	Leu	Val	His	Leu	Met	Lys	Pro	Asn	Ala	Val	Pro	Lys
	50					55			60						
Ala	Cys	Cys	Ala	Pro	Thr	Lys	Leu	Ser	Ala	Thr	Ser	Val	Leu	Tyr	Tyr
	65				70			75					80		
Asp	Ser	Ser	Asn	Asn	Val	Ile	Leu	Arg	Lys	His	Arg	Asn	Met	Val	Val
	85					90				95					
Lys	Ala	Cys	Gly	Cys	His										
	100														

## (2) INFORMATION FOR SEQ ID NO:163:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 102 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

Cys	Gln	Met	Gln	Thr	Leu	Tyr	Ile	Asp	Phe	Lys	Asp	Leu	Gly	Trp	His
1				5					10				15		
Asp	Trp	Ile	Ile	Ala	Pro	Glu	Gly	Tyr	Gly	Ala	Phe	Tyr	Cys	Ser	Gly
	20					25				30					
Glu	Cys	Asn	Phe	Pro	Leu	Asn	Ala	His	Met	Asn	Ala	Thr	Asn	His	Ala
	35				40				45						
Ile	Val	Gln	Thr	Leu	Val	His	Leu	Leu	Glu	Pro	Lys	Lys	Val	Pro	Lys
	50				55				60						
Pro	Cys	Cys	Ala	Pro	Thr	Arg	Leu	Gly	Ala	Leu	Pro	Val	Leu	Tyr	His
	65				70			75		80					
Leu	Asn	Asp	Glu	Asn	Val	Asn	Leu	Lys	Lys	Tyr	Arg	Asn	Met	Ile	Val
		85				90				95					
Lys	Ser	Cys	Gly	Cys	His										
		100													

## (2) INFORMATION FOR SEQ ID NO:164:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 103 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

Cys	Ala	Arg	Arg	Tyr	Leu	Lys	Val	Asp	Phe	Ala	Asp	Ile	Gly	Trp	Ser
1				5					10				15		
Glu	Trp	Ile	Ile	Ser	Pro	Lys	Ser	Phe	Asp	Ala	Tyr	Tyr	Cys	Ser	Gly
	20					25				30					
Ala	Cys	Gln	Phe	Pro	Met	Pro	Lys	Ser	Leu	Lys	Pro	Ser	Asn	His	Ala
	35				40				45						
Thr	Ile	Gln	Ser	Ile	Val	Arg	Ala	Val	Gly	Val	Val	Pro	Gly	Ile	Pro
	50				55				60						
Glu	Pro	Cys	Cys	Val	Pro	Glu	Lys	Met	Ser	Ser	Leu	Ser	Ile	Leu	Phe
	65				70			75			80				

Phe Asp Glu Asn Lys Asn Val Val Leu Lys Val Tyr Pro Asn Met Thr  
85 90 95

Val Glu Ser Cys Ala Cys Arg  
100

(2) INFORMATION FOR SEQ ID NO:165:

- (i) SEQUENCE CHARACTERISTICS:

  - (A) LENGTH: 102 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

Cys Lys Lys Arg His Leu Tyr Val Glu Phe Lys Asp Val Gly Trp Gln  
 1 5 10 15

Glu Cys Pro Tyr Pro Leu Thr Glu Ile Leu Asn Gly Ser Asn His Ala  
35 40 45

Ile Leu Gln Thr Leu Val His Ser Ile Glu Pro Glu Asp Ile Pro Leu  
50 55 60

Pro Cys Cys Val Pro Thr Lys Met Ser Pro Ile Ser Met Leu Phe Tyr  
65 70 75 80

Asp Asn Asn Asp Asn Val Val Leu Arg His Tyr Glu Asn Met Ala Val  
85 90 95

Asp Glu Cys Gly Cys Arg  
100

(2) INFORMATION FOR SEQ ID NO:166:

- (i) SEQUENCE CHARACTERISTICS:

  - (A) LENGTH: 106 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

Cys Arg Ala Arg Arg Leu Tyr Val Ser Phe Arg Glu Val Gly Trp His  
 1 5 10 15

Arg Trp Val Ile Ala Pro Arg Gly Phe Leu Ala Asn Tyr Cys Gln Gly  
                  20                 25                 30

Gln Cys Ala Leu Pro Val Ala Leu Ser Gly Ser Gly Gly Pro Pro Ala  
35 40 45

Leu	Asn	His	Ala	Val	Leu	Arg	Ala	Leu	Met	His	Ala	Ala	Ala	Pro	Gly
50					55				60						
Ala	Ala	Asp	Leu	Pro	Cys	Cys	Val	Pro	Ala	Arg	Leu	Ser	Pro	Ile	Ser
65				70				75				80			
Val	Leu	Phe	Phe	Asp	Asn	Ser	Asp	Asn	Val	Val	Leu	Arg	Gln	Tyr	Glu
				85				90				95			
Asp	Met	Val	Val	Asp	Glu	Cys	Gly	Cys	Arg						
				100				105							

## (2) INFORMATION FOR SEQ ID NO:167:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 101 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

Cys	His	Arg	His	Gln	Leu	Phe	Ile	Asn	Phe	Gln	Asp	Leu	Gly	Trp	His
1				5				10					15		
Lys	Trp	Val	Ile	Ala	Pro	Lys	Gly	Phe	Met	Ala	Asn	Tyr	Cys	His	Gly
			20				25					30			
Glu	Cys	Pro	Phe	Ser	Met	Thr	Thr	Tyr	Leu	Asn	Ser	Ser	Asn	Tyr	Ala
			35				40				45				
Phe	Met	Gln	Ala	Leu	Met	His	Met	Ala	Asp	Pro	Lys	Val	Pro	Lys	Ala
			50			55					60				
Val	Cys	Val	Pro	Thr	Lys	Leu	Ser	Pro	Ile	Ser	Met	Leu	Tyr	Gln	Asp
65				70			75				80				
Ser	Asp	Lys	Asn	Val	Ile	Leu	Arg	His	Tyr	Glu	Asp	Met	Val	Val	Asp
			85			90					95				
Glu	Cys	Gly	Cys	Gly											
			100												

## (2) INFORMATION FOR SEQ ID NO:168:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 103 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

Cys	Arg	Arg	Thr	Ser	Leu	His	Val	Asn	Phe	Lys	Glu	Ile	Gly	Trp	Asp
1					5			10				15			

Ser Trp Ile Ile Ala Pro Lys Asp Tyr Glu Ala Phe Glu Cys Lys Gly  
 20 25 30  
 Gly Cys Phe Phe Pro Leu Thr Asp Asn Val Thr Pro Thr Lys His Ala  
 35 40 45  
 Ile Val Gln Thr Leu Val His Leu Gln Asn Pro Lys Lys Ala Ser Lys  
 50 55 60  
 Ala Cys Cys Val Pro Thr Lys Leu Asp Ala Ile Ser Ile Leu Tyr Lys  
 65 70 75 80  
 Asp Asp Ala Gly Val Pro Thr Leu Ile Tyr Asn Tyr Glu Gly Met Lys  
 85 90 95  
 Val Ala Glu Cys Gly Cys Arg  
 100

## (2) INFORMATION FOR SEQ ID NO:169:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 105 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

Cys His Arg Val Ala Leu Asn Ile Ser Phe Gln Glu Leu Gly Trp Glu  
 1 5 10 15  
 Arg Trp Ile Val Tyr Pro Pro Ser Phe Ile Phe His Tyr Cys His Gly  
 20 25 30  
 Gly Cys Gly Leu His Ile Pro Pro Asn Leu Ser Leu Pro Val Pro Gly  
 35 40 45  
 Ala Pro Pro Thr Pro Ala Gln Pro Tyr Ser Leu Leu Pro Gly Ala Gln  
 50 55 60  
 Pro Cys Cys Ala Ala Leu Pro Gly Thr Met Arg Pro Leu His Val Arg  
 65 70 75 80  
 Thr Thr Ser Asp Gly Gly Tyr Ser Phe Lys Tyr Glu Thr Val Pro Asn  
 85 90 95  
 Leu Leu Thr Gln His Cys Ala Cys Ile  
 100 105

## (2) INFORMATION FOR SEQ ID NO:170:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 99 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

Cys Ala Leu Arg Glu Leu Ser Val Asp Leu Arg Ala Glu Arg Ser Val  
 1                   5                   10                   15  
 Leu Ile Pro Glu Thr Tyr Gln Ala Asn Asn Cys Gln Gly Ala Cys Gly  
 20                 25                 30  
 Trp Pro Gln Ser Asp Arg Asn Pro Arg Tyr Gly Asn His Val Val Leu  
 35                 40                 45  
 Leu Leu Lys Met Gln Ala Arg Gly Ala Thr Leu Ala Arg Pro Pro Cys  
 50                 55                 60  
 Cys Val Pro Thr Ala Tyr Thr Gly Lys Leu Leu Ile Ser Leu Ser Glu  
 65                 70                 75                 80  
 Glu Arg Ile Ser Ala His His Val Pro Asn Met Val Ala Thr Glu Cys  
 85                 90                 95  
 Gly Cys Arg

## (2) INFORMATION FOR SEQ ID NO:171:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 102 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

Cys Glu Leu His Asp Phe Ser Leu Ser Phe Ser Gln Leu Lys Trp Asp  
 1                 5                 10                 15  
 Asn Trp Ile Val Ala Pro His Ser Tyr Asn Pro Ser Tyr Cys Lys Gly  
 20                 25                 30  
 Asp Cys Pro Ser Ala Val Ser His Arg Tyr Gly Ser Pro Val His Thr  
 35                 40                 45  
 Met Val Gln Asn Met Ile Tyr Glu Lys Leu Asp Pro Ser Val Pro Ser  
 50                 55                 60  
 Pro Ser Cys Val Pro Gly Lys Tyr Ser Pro Leu Ser Val Leu Thr Ile  
 65                 70                 75                 80  
 Glu Pro Asp Gly Ser Ile Ala Tyr Lys Glu Tyr Glu Asp Met Met Ala  
 85                 90                 95  
 Thr Ser Cys Thr Cys Arg  
 100

## (2) INFORMATION FOR SEQ ID NO:172:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 94 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

Cys Val Leu Thr Ala Ile His Leu Asn Val Thr Asp Leu Gly Leu Gly  
1 5 10 15

Tyr Glu Thr Lys Glu Glu Leu Ile Phe Arg Tyr Cys Ser Gly Ser Cys  
20 25 30

Asp Ala Ala Glu Thr Thr Tyr Asp Lys Ile Leu Lys Asn Leu Ser Arg  
35 40 45

Asn Arg Arg Leu Val Ser Asp Lys Val Gly Gln Ala Cys Cys Arg Pro  
50 55 60

Ile Ala Phe Asp Asp Asp Leu Ser Phe Leu Asp Asp Asn Leu Val Tyr  
65 70 75 80

His Ile Leu Arg Lys His Ser Ala Lys Arg Cys Gly Cys Ile  
85 90

(2) INFORMATION FOR SEQ ID NO:173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

Cys Gly Leu Arg Glu Leu Glu Val Arg Val Ser Glu Leu Gly Leu Gly  
1 5 10 15

Tyr Ala Ser Asp Glu Thr Val Leu Phe Arg Tyr Cys Ala Gly Ala Cys  
20 25 30

Glu Ala Ala Ala Arg Val Tyr Asp Leu Gly Leu Arg Arg Leu Arg Gln  
35 40 45

Arg Arg Arg Leu Arg Arg Glu Arg Val Arg Ala Gln Pro Cys Cys Arg  
50 55 60

Pro Thr Ala Tyr Glu Asp Glu Val Ser Phe Leu Asp Ala His Ser Arg  
65 70 75 80

Tyr His Thr Val His Glu Leu Ser Ala Arg Glu Cys Ala Cys Val  
85 90 95

(2) INFORMATION FOR SEQ ID NO:174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

Leu	Asp	Leu	Gln	Glu	Ala	Ser	Val	Ala	Asp	Lys	Leu	Ser	Phe	Gly	Lys
1				5				10						15	

  

Met	Ala	Glu	Thr	Arg	Gly	Thr	Trp	Thr	Pro	His	Gln	Gly	Asn	Asn	His
				20				25					30		

  

Val	Arg	Leu	Pro	Arg											
				35											

(2) INFORMATION FOR SEQ ID NO:175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

Leu	Asp	Leu	Gln	Glu	Ala	Pro	Ala	Ala	Asp	Glu	Leu	Ser	Ser	Gly	Lys
1					5				10					15	

  

Met	Ala	Glu	Thr	Gly	Arg	Thr	Trp	Lys	Pro	His	Gln	Gly	Asn	Asn	Asn
				20				25					30		

  

Val	Arg	Leu	Pro	Arg											
				35											

(2) INFORMATION FOR SEQ ID NO:176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

Cys	Val	Leu	Thr	Ala	Ile	His	Leu	Asn	Val	Thr	Asp	Leu	Gly	Leu	Gly
1					5				10					15	

  

Tyr	Glu	Thr	Lys	Glu	Glu	Leu	Ile	Phe	Arg	Tyr	Cys	Ser	Gly	Ser	Cys
				20				25					30		

  

Glu	Ser	Ala	Glu	Thr	Met	Tyr	Asp	Lys	Ile	Leu	Lys	Asn	Leu	Ser	Arg
					35			40					45		

Ser	Arg	Arg	Leu	Thr	Ser	Asp	Lys	Val	Gly	Gln	Ala	Cys	Cys	Arg	Pro
50							55				60				
Val	Ala	Phe	Asp	Asp	Asp	Leu	Ser	Phe	Leu	Asp	Asp	Asn	Leu	Val	Tyr
65						70				75				80	
His	Ile	Leu	Arg	Lys	His	Ser	Ala	Lys	Arg	Cys	Gly	Cys			
						85				90					

## (2) INFORMATION FOR SEQ ID NO:177:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 723 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

ATGGCTGCAG	GAAGACTTCG	GATCCTGTGT	CTGCTGCTCC	TGTCCTTGCA	CCCGAGCCTC	60
GGCTGGGTCC	TTGATCTTCA	AGAGGCTTCT	GTGGCAGATA	AGCTCTCATT	TGGGAAGATG	120
GCAGAGACTA	GAGGGACCTG	GACGCCCAT	CAGGGTAAGA	ATT CCTGGGG	GCCTCCCGAC	180
TCCCCAATTC	CTTCTCTCAA	AGCCCTCACT	TTGCCTTACA	ATCCTACTCT	ACCTTGCACT	240
AGGTAACAAAC	CATGTCCGTC	TTCCAAGAGC	CTTGGCTGGT	TCATGCCGAC	TGTGGAGCCT	300
GACCCTACCA	GTGGCTGAGC	TGGGCCTGGG	CTATGCCCTG	GAGGAGAAGG	TCATCTTCCG	360
ATACTGTGCT	GGCAGCTGTC	CCCAAGAGGC	CCGTACCCAG	CACAGTCTGG	TACTGGCCCG	420
GCTTCGAGGG	CGGGGTCGAG	CCCATGGCCG	ACCCTGCTGC	CAGCCCACCA	GCTATGCTGA	480
TGTGACCTTC	CTTGATGATC	AGCACCAATTG	GCAGCAGCTG	CCTCAGCTCT	CAGCTGCAGC	540
TTGTGGCTGT	GGTGGCTGAA	GGAGGCCAGT	CTGGTGTCTC	AGAACACAA	GCATGAGACA	600
GGCTGGGCTT	TGAAAGGCTC	AGGTGACATT	ACTAGAAATT	TGCATAGGTA	AAGATAAGAA	660
GGGAAAGGAC	CAGGGTTTT	TTGTTTCTTT	CTTTGCTTGC	TTGTTAGTTT	TTTTTTTTT	720
TTT						723

## (2) INFORMATION FOR SEQ ID NO:178:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 723 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

AAAAAAAAAAA	AAAAAACTAA	CAAGCAAGCA	AAGAAAGAAA	AAAAAAACCC	CTGGTCCTTT	60
-------------	------------	------------	------------	------------	------------	----

CCCTTCTTAT	CTTTACCTAT	GCAAATTCT	AGTAATGTCA	CCTGAGCCTT	TCAAAGCCCA	120
GCCTGTCTCA	TGCTTGAT	TCTGAGACAC	CAGACTGGCC	TCCTTCAGCC	ACCACAGCCA	180
CAAGCTGCAG	CTGAGAGCTG	AGGCAGCTGC	TGCCAATGGT	GCTGATCATC	AAGGAAGGTC	240
ACATCAGCAT	AGCTGGTGGG	CTGGCAGCAG	GGTCGGCCAT	GGGCTCGACC	CCGCCCTCGA	300
AGCCGGGCCA	GTACCAGACT	GTGCTGGTA	CGGGCCTCTT	GGGGACAGCT	GCCAGCACAG	360
TATCGGAAGA	TGACCTTCTC	CTCCGAGGCA	TAGCCCAGGC	CCAGCTCAGC	CACTGGTAGG	420
GTCAAGGCTCC	ACAGTCGGCA	TGAACCAGCC	AAGGCTCTTG	GAAGACGGAC	ATGGTTGTTA	480
CCTAGTGCAA	GGTAGAGTAG	GATTGTAAGG	CAAAGTGAGG	GCTTGAGAG	AAGGAATTGG	540
GGAGTCGGGA	GGCCCCCAGG	AATTCTTACC	CTGATGGGGC	GTCCAGGTCC	CTCTAGTCTC	600
TGCCATCTTC	CCAAATGAGA	GCTTATCTGC	CACAGAACCC	TCTTGAAGAT	CAAGGACCCA	660
GCCGAGGCTC	GGGTGCAAGG	ACAGGAGCAG	CAGACACAGG	ATCCGAAGTC	TTCCCTGCAGC	720
CAT						723

## (2) INFORMATION FOR SEQ ID NO:179:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 471 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

ATGGCTGCAG	GAAGACTTCG	GATCCTGTGT	CTGCTGCTCC	TGTCTTGCA	CCCGAGCCTC	60
GGCTGGGTCC	TTGATCTTCA	AGAGGCTTCT	GTGGCAGATA	AGCTCTCATT	TGGGAAGATG	120
GCAGAGACTA	GAGGGACCTG	GACGCCCAT	CAGGGTAACA	ACCATGTCCG	TCTTCCAAGA	180
GCCTTGGCTG	GTTCATGCCG	ACTGTGGAGC	CTGACCCCTAC	CAGTGGCTGA	GCTGGGCCTG	240
GGCTATGCCT	CGGAGGAGAA	GGTCATCTTC	CGATACTGTG	CTGGCAGCTG	TCCCCAAGAG	300
GCCC GTACCC	AGCACAGTCT	GGTACTGGCC	CGGCTTCGAG	GGCGGGGTCG	AGCCCATGGC	360
CGACCCCTGCT	GCCAGCCCAC	CAGCTATGCT	GATGTGACCT	TCCTTGATGA	TCAGCACCAT	420
TGGCAGCAGC	TGCCTCAGCT	CTCAGCTGCA	GCTTGTGGCT	GTGGTGGCTG	A	471

## (2) INFORMATION FOR SEQ ID NO:180:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 471 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

TCAGGCCACCA CAGCCACAAG CTGCAGCTGA GAGCTGAGGC AGCTGCTGCC	AATGGTGCTG 60
ATCATCAAGG AAGGTCACAT CAGCATAAGCT GGTGGGCTGG CAGCAGGGTC	GGCCATGGGC 120
TCGACCCCCGC CCTCGAAGCC GGGCCAGTAC CAGACTGTGC TGGGTACGGG	CCTCTTGGGG 180
ACAGCTGCCA GCACAGTATC GGAAGATGAC CTTCTCCTCC GAGGCATAGC	CCAGGCCAG 240
CTCAGCCACT GGTAGGGTCA GGCTCCACAG TCGGCATGAA CCAGCCAAGG	CTCTTGAAG 300
ACGGACATGG TTGTTACCT GATGGGGCGT CCAGGTCCCT CTAGTCTCTG	CCATCTTCCC 360
AAATGAGAGC TTATCTGCCA CAGAACCTC TTGAAGATCA AGGACCCAGC	CGAGGCTCGG 420
GTGCAAGGAC AGGAGCAGCA GACACAGGAT CGAAGTCTT CCTGCAGCCA	T 471

## (2) INFORMATION FOR SEQ ID NO:181:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 180 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

ATGGCTGCAG GAAGACTTCG GATCCTGTGT CTGCTGCTCC TGTCCCTGCA	CCCGAGCCTC 60
GGCTGGGTCC TTGATCTTCA AGAGGCTTCT GTGGCAGATA AGCTCTCATT	TGGGAAGATG 120
GCAGAGACTA GAGGGACCTG GACGCCCAT CAGGGTAACA ACCATGTCCG	TCTTCCAAGA 180

## (2) INFORMATION FOR SEQ ID NO:182:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 180 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

TCTTGGAAAGA CGGACATGGT TGTTACCTG ATGGGGCGTC CAGGTCCCTC	TAGTCTCTGC 60
CATCTTCCCA AATGAGAGCT TATCTGCCAC AGAACCTCT TGAAGATCAA	GGACCCAGCC 120
GAGGCTCGGG TGCAAGGACA GGAGCAGCAG ACACAGGATC CGAAGTCTTC	CTGCAGCCAT 180

## (2) INFORMATION FOR SEQ ID NO:183:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

GCCTTGGCTG GTTCATGCCG ACTGTGGAGC CTGACCCCTAC CAGTGGCTGA GCTGGGCCTG	60
GGCTATGCCT CGGAGGAGAA GGTCACTTTC CGATACTGTG CTGGCAGCTG TCCCCAAGAG	120
GCCCCGTACCC AGCACAGTCT GGTACTGGCC CGGCTTCGAG GGCGGGGTCG AGCCCATGGC	180
CGACCCTGCT GCCAGCCCCAC CAGCTATGCT GATGTGACCT TCCTTGATGA TCAGCACCAT	240
TGGCAGCAGC TGCCTCAGCT CTCAGCTGCA GCTTGTGGCT GTGGTGGCTG A	291

(2) INFORMATION FOR SEQ ID NO:184:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 291 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

TCAGGCCACCA CAGCCACAAG CTGCAGCTGA GAGCTGAGGC AGCTGCTGCC AATGGTGCTG	60
ATCATCAAGG AAGGTACACAT CAGCATAGCT GGTGGGCTGG CAGCAGGGTC GGCCATGGGC	120
TCGACCCCCGC CCTCGAACGCC GGGCCAGTAC CAGACTGTGC TGGGTACGGG CCTCTTGGGG	180
ACAGCTGCCA GCACAGTATC GGAAGATGAC CTTCTCCTCC GAGGCATAGC CCAGGCCCCAG	240
CTCAGCCACT GGTAGGGTCA GGCTCCACAG TCGGCATGAA CCAGCCAAGG C	291

(2) INFORMATION FOR SEQ ID NO:185:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 156 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

Met Ala Ala Gly Arg Leu Arg Ile Leu Cys Leu Leu Leu Ser Leu	
1 5 10 15	

His Pro Ser Leu Gly Trp Val Leu Asp Leu Gln Glu Ala Ser Val Ala

20	25	30
Asp Lys Leu Ser Phe Gly Lys Met Ala Glu Thr Arg Gly Thr Trp Thr		
35	40	45
Pro His Gln Gly Asn Asn His Val Arg Leu Pro Arg Ala Leu Ala Gly		
50	55	60
Ser Cys Arg Leu Trp Ser Leu Thr Leu Pro Val Ala Glu Leu Gly Leu		
65	70	75
Gly Tyr Ala Ser Glu Glu Lys Val Ile Phe Arg Tyr Cys Ala Gly Ser		
85	90	95
Cys Pro Gln Glu Ala Arg Thr Gln His Ser Leu Val Leu Ala Arg Leu		
100	105	110
Arg Gly Arg Gly Arg Ala His Gly Arg Pro Cys Cys Gln Pro Thr Ser		
115	120	125
Tyr Ala Asp Val Thr Phe Leu Asp Asp Gln His His Trp Gln Gln Leu		
130	135	140
Pro Gln Leu Ser Ala Ala Ala Cys Gly Cys Gly Gly		
145	150	155

## (2) INFORMATION FOR SEQ ID NO:186:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 60 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
  
- (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

1	5	10
Met Ala Ala Gly Arg Leu Arg Ile Leu Cys Leu Leu Leu Ser Leu		
15		
His Pro Ser Leu Gly Trp Val Leu Asp Leu Gln Glu Ala Ser Val Ala		
20	25	30
Asp Lys Leu Ser Phe Gly Lys Met Ala Glu Thr Arg Gly Thr Trp Thr		
35	40	45
Pro His Gln Gly Asn Asn His Val Arg Leu Pro Arg		
50	55	60

## (2) INFORMATION FOR SEQ ID NO:187:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 96 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
  
- (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

Ala	Leu	Ala	Gly	Ser	Cys	Arg	Leu	Trp	Ser	Leu	Thr	Leu	Pro	Val	Ala
1					5					10					15
Glu	Leu	Gly	Leu	Gly	Tyr	Ala	Ser	Glu	Glu	Lys	Val	Ile	Phe	Arg	Tyr
					20				25						30
Cys	Ala	Gly	Ser	Cys	Pro	Gln	Glu	Ala	Arg	Thr	Gln	His	Ser	Leu	Val
					35				40						45
Leu	Ala	Arg	Leu	Arg	Gly	Arg	Gly	Arg	Ala	His	Gly	Arg	Pro	Cys	Cys
					50			55			60				
Gln	Pro	Thr	Ser	Tyr	Ala	Asp	Val	Thr	Phe	Leu	Asp	Asp	Gln	His	His
					65			70			75				80
Trp	Gln	Gln	Leu	Pro	Gln	Leu	Ser	Ala	Ala	Ala	Cys	Gly	Cys	Gly	Gly
					85				90						95

## (2) INFORMATION FOR SEQ ID NO:188:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 559 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

ATGGCTGCAG	GAAGACTTCG	GATCTTGT	TT CTGCTGCTCC	TGTCCTTGCA	CCTGGGCCTT	60
GGCTGGGTCC	TTGATCTTCA	AGAGGCTCCT	GCGGCAGATG	AGCTCTCATC	TGGGAAAATG	120
GCAGAGACTG	GAAGGACCTG	GAAGCCCCAT	CAGGGTAAGA	ATTCTTGGGG	GCCTCCTAAC	180
TCTACAGTTC	TTCCCTCTCAA	AGCCCTCACT	TTGCCTCAC	ATCCTATTCT	ACCTTGCACT	240
AGGTAACAAAC	AATGTCCGCC	TTCCAAGAGC	CTTACCTGGT	TTGTGCCGGC	TGTGGAGCCT	300
GACCCTACCA	GTGGCTGAGC	TTGGCCTGGG	CTATGCCTCA	GAGGAGAAGA	TTATCTTCCG	360
ATACTGTGCT	GGCAGCTGTC	CCCAAGAGGT	CCGTACCCAG	CACAGTCTGG	TGCTGGCCCG	420
TCTTCGAGGG	CAGGGTCGAG	CTCATGGCAG	ACCTTGCTGC	CAGCCCACCA	GCTATGCTGA	480
TGTGACCTTC	CTTGATGACC	ACCACCATTG	GCAGCAGCTG	CCTCAGCTCT	CAGCCGCAGC	540
TTGTGGCTGT	GGTGGCTGA					559

## (2) INFORMATION FOR SEQ ID NO:189:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 559 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

TCAGGCCACCA CAGCCACAAG CTGCGGCTGA GAGCTGAGGC AGCTGCTGCC AATGGTGGTG	60
GTCATCAAGG AAGGTACAT CAGCATAGCT GGTGGGCTGG CAGCAAGGTC TGCCATGAGC	120
TCGACCCTGC CCTCGAAGAC GGGCCAGCAC CAGACTGTGC TGGGTACCGA CCTCTGGGG	180
ACAGCTGCCA GCACAGTATC GGAAGATAAT CTTCTCCTCT GAGGCATAGC CCAGGCCAAG	240
CTCAGCCACT GGTAGGGTCA GGCTCCACAG CCGGCACAAA CCAGGTAAGG CTCTTGGAAAG	300
GCGGACATTG TTGTTACCTA GTGCAAGGTA GAATAGGATT GTGAGGCAA GTGAGGGCTT	360
TGAGAGGAAG AACTGTAGAG TTAGGAGGCC CCCAAGAATT CTTACCCCTGA TGGGGCTTCC	420
AGGTCTTCC AGTCTCTGCC ATTTTCCCAG ATGAGAGCTC ATCTGCCGCA GGAGCCTCTT	480
GAAGATCAAG GACCCAGCCA AGGCCAGGT GCAAGGACAG GAGCAGCAGA AACAAAGATCC	540
GAAGTCTTCC TGCAGCCAT	559

## (2) INFORMATION FOR SEQ ID NO:190:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 471 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

ATGGCTGCAG GAAGACTTCG GATCTGTTT CTGCTGCTCC TGTCTTGCA CCTGGGCCTT	60
GGCTGGGTCC TTGATCTTCA AGAGGCTCCT GCGGCAGATG AGCTCTCATC TGGGAAAATG	120
GCAGAGACTG GAAGGACCTG GAAGCCCCAT CAGGGTAACA ACAATGTCCG CCTTCCAAGA	180
GCCTTACCTG GTTTGTGCCG GCTGTGGAGC CTGACCTAC CAGTGGCTGA GCTTGGCCTG	240
GGCTATGCCT CAGAGGAGAA GATTATCTTC CGATACTGTG CTGGCAGCTG TCCCCAAGAG	300
GTCCGTACCC AGCACAGTCT GGTGCTGGCC CGTCTTCGAG GGCAGGGTCG AGCTCATGGC	360
AGACCTTGCT GCCAGCCCAC CAGCTATGCT GATGTGACCT TCCTTGATGA CCACCAACCAT	420
TGGCAGCAGC TGCCTCAGCT CTCAGCCGCA GCTTGTGGCT GTGGTGGCTG A	471

## (2) INFORMATION FOR SEQ ID NO:191:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 471 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

TCAGGCCACCA CAGCCACAAG CTGCGGCTGA GAGCTGAGGC AGCTGCTGCC AATGGTGGTG	60
GTCATCAAGG AAGGTACAT CAGCATAGCT GGTGGGCTGG CAGCAAGGTC TGCCATGAGC	120
TCGACCCTGC CCTCGAAGAC GGGCCAGCAC CAGACTGTGC TGGGTACGGA CCTCTTGGGG	180
ACAGCTGCCA GCACAGTATC GGAAGATAAT CTTCTCCTCT GAGGCATAGC CCAGGCCAAG	240
CTCAGCCACT GGTAGGGTCA GGCTCCACAG CGGGCACAAA CCAGGTAAGG CTCTTGGAAAG	300
GCGGACATTG TTGTTACCT GATGGGGCTT CCAGGTCTT CCAGTCTCTG CCATTTCCC	360
AGATGAGAGC TCATCTGCCG CAGGAGCCTC TTGAAGATCA AGGACCCAGC CAAGGCCAG	420
GTGCAAGGAC AGGAGCAGCA GAAACAAGAT CCGAAGTCTT CCTGCAGCCA T	471

## (2) INFORMATION FOR SEQ ID NO:192:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 180 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

ATGGCTGCAG GAAGACTTCG GATCTTGTTC CTGCTGCTCC TGTCCCTGCA CCTGGGCCTT	60
GGCTGGGTCC TTGATCTTCA AGAGGCTCCT GCGGCAGATG AGCTCTCATC TGGGAAAATG	120
GCAGAGACTG GAAGGACCTG GAAGCCCCAT CAGGGTAACA ACAATGTCCG CCTTCCAAGA	180

## (2) INFORMATION FOR SEQ ID NO:193:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 180 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

TCTTGGAAAGG CGGACATTGT TGTTACCTG ATGGGGCTTC CAGGTCTTC CAGTCTCTGC	60
CATTTTCCCA GATGAGAGCT CATCTGCCGC AGGAGCCTCT TGAAGATCAA GGACCCAGCC	120
AAGGCCAGG TGCAAGGACA GGAGCAGCAG AAACAAGATC CGAAGTCTTC CTGCAGCCAT	180

## (2) INFORMATION FOR SEQ ID NO:194:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

GCCTTACCTG GTTGTCGCCG GCTGTGGAGC CTGACCCCTAC CAGTGGCTGA GCTTGGCCTG	60
GGCTATGCCT CAGAGGAGAA GATTATCTTC CGATACTGTG CTGGCAGCTG TCCCCAAGAG	120
GTCCGTACCC AGCACAGTCT GGTGCTGGCC CGTCTTCGAG GGCAGGGTCG AGCTCATGGC	180
AGACCTTGCT GCCAGCCCAC CAGCTATGCT GATGTGACCT TCCTTGATGA CCACCACCAT	240
TGGCAGCAGC TGCCTCAGCT CTCAGCCGCA GCTTGTGGCT GTGGTGGCTG A	291

(2) INFORMATION FOR SEQ ID NO:195:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 291 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

TCAGCCACCA CAGCCACAAG CTGCGGCTGA GAGCTGAGGC AGCTGCTGCC AATGGTGGTG	60
GTCATCAAGG AAGGTACAT CAGCATAGCT GGTGGGCTGG CAGCAAGGTC TGCCATGAGC	120
TCGACCCCTGC CCTCGAACAG GGGCCAGCAC CAGACTGTGC TGGGTACGGA CCTCTTGGGG	180
ACAGCTGCCA GCACAGTATC GGAAGATAAT CTTCTCCTCT GAGGCATAGC CCAGGCCAAG	240
CTCAGCCACT GGTAGGGTCA GGCTCCACAG CCGGCACAAA CCAGGTAAGG C	291

(2) INFORMATION FOR SEQ ID NO:196:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 156 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

Met Ala Ala Gly Arg Leu Arg Ile Leu Phe Leu Leu Leu Ser Leu			
1	5	10	15

His Leu Gly Leu Gly Trp Val Leu Asp Leu Gln Glu Ala Pro Ala Ala  
 20 25 30

Asp Glu Leu Ser Ser Gly Lys Met Ala Glu Thr Gly Arg Thr Trp Lys  
 35 40 45

Pro His Gln Gly Asn Asn Asn Val Arg Leu Pro Arg Ala Leu Pro Gly  
 50 55 60

Leu Cys Arg Leu Trp Ser Leu Thr Leu Pro Val Ala Glu Leu Gly Leu  
 65 70 75 80

Gly Tyr Ala Ser Glu Glu Lys Ile Ile Phe Arg Tyr Cys Ala Gly Ser  
 85 90 95

Cys Pro Gln Glu Val Arg Thr Gln His Ser Leu Val Leu Ala Arg Leu  
 100 105 110

Arg Gly Gln Gly Arg Ala His Gly Arg Pro Cys Cys Gln Pro Thr Ser  
 115 120 125

Tyr Ala Asp Val Thr Phe Leu Asp Asp His His His Trp Gln Gln Leu  
 130 135 140

Pro Gln Leu Ser Ala Ala Ala Cys Gly Cys Gly Gly  
 145 150 155

## (2) INFORMATION FOR SEQ ID NO:197:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 60 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

Met Ala Ala Gly Arg Leu Arg Ile Leu Phe Leu Leu Leu Leu Ser Leu  
 1 5 10 15

His Leu Gly Leu Gly Trp Val Leu Asp Leu Gln Glu Ala Pro Ala Ala  
 20 25 30

Asp Glu Leu Ser Ser Gly Lys Met Ala Glu Thr Gly Arg Thr Trp Lys  
 35 40 45

Pro His Gln Gly Asn Asn Asn Val Arg Leu Pro Arg  
 50 55 60

## (2) INFORMATION FOR SEQ ID NO:198:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 96 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

Ala	Leu	Pro	Gly	Leu	Cys	Arg	Leu	Trp	Ser	Leu	Thr	Leu	Pro	Val	Ala
1				5					10						15
Glu	Leu	Gly	Leu	Gly	Tyr	Ala	Ser	Glu	Glu	Lys	Ile	Ile	Phe	Arg	Tyr
	20							25							30
Cys	Ala	Gly	Ser	Cys	Pro	Gln	Glu	Val	Arg	Thr	Gln	His	Ser	Leu	Val
	35						40								45
Leu	Ala	Arg	Leu	Arg	Gly	Gln	Gly	Arg	Ala	His	Gly	Arg	Pro	Cys	Cys
	50					55									60
Gln	Pro	Thr	Ser	Tyr	Ala	Asp	Val	Thr	Phe	Leu	Asp	Asp	His	His	His
	65					70			75						80
Trp	Gln	Gln	Leu	Pro	Gln	Leu	Ser	Ala	Ala	Ala	Cys	Gly	Cys	Gly	Gly
					85				90						95

## (2) INFORMATION FOR SEQ ID NO:199:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 291 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

GCCCTGTCTG	GTCCATGCCA	GCTGTGGAGC	CTGACCCCTGT	CCGTGGCAGA	GCTAGGCCTG	60
GGCTACGCCT	CAGAGGAGAA	GGTCATCTTC	CGCTACTGCG	CCGGCAGCTG	CCCCCGTGGT	120
GCCCACCC	AGCATGGCCT	GGCGCTGGCC	CGGCTGCAGG	GCCAGGGCCG	AGCCCACGGT	180
GGGCCCTGCT	GCCGGCCCAC	TCGCTACACC	GACGTGGCCT	TCCTCGATGA	CCGCCACCGC	240
TGGCAGCGGC	TGCCCCAGCT	CTCGGCGGCT	GCCTGCGGCT	GTGGTGGCTG	A	291

## (2) INFORMATION FOR SEQ ID NO:200:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 291 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

TCAGCCACCA	CAGCCGCAGG	CAGCCGCCGA	GAGCTGGGGC	AGCCGCTGCC	AGCGGTGGCG	60
GTCATCGAGG	AAGGCCACGT	CGGTGTAGCG	AGTGGGCCGG	CAGCAGGGCC	CACCGTGGGC	120

TCGGCCCTGG CCCTGCAGCC GGGCCAGCGC CAGGCCATGC TGGGTGCGGG CACCACGGGG	180
GCAGCTGCCG GCGCAGTAGC GGAAGATGAC CTTCTCCTCT GAGGCGTAGC CCAGGCCTAG	240
CTCTGCCACG GACAGGGTCA GGCTCCACAG CTGGCATGGA CCAGACAGGG C	291

## (2) INFORMATION FOR SEQ ID NO:201:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 291 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

GCCCTGTCTG GTCCATGCCA GCTGTGGAGC CTGACCCTGT CCGTGGCAGA GCTAGGCCTG	60
GGCTACGCCT CAGAGGAGAA GGTCACTTTC CGCTACTGCG CGGGCAGCTG CCCCCGTGGT	120
GCCCGCACCC AGCATGGCCT GGCGCTGGCC CGGCTGCAGG GCCAGGGCCG AGCCCACGGC	180
GGGCCCTGCT GCCGGCCAC TCGCTACACC GACGTGGCCT TCCTCGATGA CCGCCACCGC	240
TGGCAGCGGC TGCCCCAGCT CTCGGCGGCT GCCTGCGGCT GTGGTGGCTG A	291

## (2) INFORMATION FOR SEQ ID NO:202:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 291 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

TCAGCCACCA CAGCCGCAGG CAGCCGCCGA GAGCTGGGGC AGCCGCTGCC AGCGGTGGCG	60
GTCATCGAGG AAGGCCACGT CGGTGTAGCG AGTGGGCCGG CAGCAGGGCC CGCCGTGGC	120
TCGGCCCTGG CCCTGCAGCC GGGCCAGCGC CAGGCCATGC TGGGTGCGGG CACCACGGGG	180
GCAGCTGCCG GCGCAGTAGC GGAAGATGAC CTTCTCCTCT GAGGCGTAGC CCAGGCCTAG	240
CTCTGCCACG GACAGGGTCA GGCTCCACAG CTGGCATGGA CCAGACAGGG C	291

## (2) INFORMATION FOR SEQ ID NO:203:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 471 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

ATGGCCGTAG	GGAAGTCCT	GCTGGGCTCT	CTGCTGCTCC	TGTCCCTGCA	GCTGGGACAG	60
GGCTGGGCC	CCGATGCCCG	TGGGGTCCC	GTGGCCGATG	GAGAGTTCTC	GTCTGAACAG	120
GTGGCAAAGG	CTGGAGGGAC	CTGGCTGGC	ACCCACCGCC	CCCTTGCCCG	CCTGCGCCGA	180
GCCCTGTCTG	GTCCATGCCA	GCTGTGGAGC	CTGACCCGT	CCGTGGCAGA	GCTAGGCCTG	240
GGCTACGCCT	CAGAGGAGAA	GGTCATCTTC	CGCTACTGCG	CCGGCAGCTG	CCCCCGTGGT	300
GCCCGCACCC	AGCATGGCCT	GGCGCTGGCC	CGGCTGCAGG	GCCAGGGCCG	AGCCCACGGT	360
GGGCCCTGCT	GCCGGCCAC	TCGCTACACC	GACGTGGCCT	TCCTCGATGA	CCGCCACCGC	420
TGGCAGCGGC	TGCCCCAGCT	CTCGGCGGCT	GCCTGCGGCT	GTGGTGGCTG	A	471

## (2) INFORMATION FOR SEQ ID NO:204:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 471 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

TCAGCCACCA	CAGCCGCAGG	CAGCCGCCGA	GAGCTGGGC	AGCCGCTGCC	AGCGGTGGCG	60
GTCATCGAGG	AAGGCCACGT	CGGTGTAGCG	AGTGGGCCGG	CAGCAGGGCC	CACCGTGGGC	120
TCGGCCCTGG	CCCTGCAGCC	GGGCCAGCGC	CAGGCCATGC	TGGGTGCGGG	CACCACGGGG	180
GCAGCTGCCG	GCGCAGTAGC	GGAAGATGAC	CTTCTCCTCT	GAGGCGTAGC	CCAGGCCTAG	240
CTCTGCCACG	GACAGGGTCA	GGCTCCACAG	CTGGCATGGA	CCAGACAGGG	CTCGGCGCAG	300
GCGGGCAAGG	GGGCGGTGGG	TGCCAGCCA	GGTCCCTCCA	GCCTTGCCA	CCTGTTCAGA	360
CGAGAACTCT	CCATCGGCCA	CGGGAACCCC	ACGGGCATCG	GGGCCCCAGC	CCTGTCCCAG	420
CTGCAGGGAC	AGGAGCAGCA	GAGAGCCCAG	CAGGAACCTTC	CCTACGGCCA	T	471

## (2) INFORMATION FOR SEQ ID NO:205:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 471 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

ATGGCCGTAG GGAAGTCCT GCTGGCTCC CTGCTGCTCC TGTCCCTGCA GCTGGGACAG	60
GGCTGGGGCC CCGATGCCCG TGGGGTCCC GTGGCCGATG GAGAGTTCTC GTCTGAACAG	120
GTGGCAAAGG CTGGAGGGAC CTGGCTGGC ACCCACCGCC CCCTTGCCCG CCTGCGCCGA	180
GCCCTGTCTG GTCCATGCCA GCTGTGGAGC CTGACCCGTG CCGTGGCAGA GCTAGGCCTG	240
GGCTACGCCT CAGAGGAGAA GGTCATCTTC CGCTACTGCG CCGGCAGCTG CCCCCGTGGT	300
GCCCCCACCC AGCATGGCCT GGCCTGGCC CGGCTGCAGG GCCAGGGCCG AGCCCACGGC	360
GGGCCCTGCT GCCGGCCAC TCGCTACACC GACGTGGCCT TCCTCGATGA CCGCCACCGC	420
TGGCAGCGGC TGCCCCAGCT CTCGGCGGCT GCCTGCGGCT GTGGTGGCTG A	471

## (2) INFORMATION FOR SEQ ID NO:206:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 471 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

TCAGCCACCA CAGCCGCAGG CAGCCGCCGA GAGCTGGGGC AGCCGCTGCC AGCGGTGGCG	60
GTCATCGAGG AAGGCCACGT CGGTGTAGCG AGTGGGCCGG CAGCAGGGCC CGCCGTGGC	120
TCGGCCCTGG CCCTGCAGCC GGGCCAGCGC CAGGCCATGC TGGGTGCGGG CACCACGGG	180
GCAGCTGCCG GCGCAGTAGC GGAAGATGAC CTTCTCCTCT GAGGCGTAGC CCAGGCCTAG	240
CTCTGCCACG GACAGGGTCA GGCTCCACAG CTGGCATGGA CCAGACAGGG CTCGGCGCAG	300
GGGGGCAAGG GGGCGGTGGG TGCCCAGCCA GGTCCCTCCA GCCTTGCCTA CCTGTTCA	360
CGAGAACTCT CCATCGGCCA CGGGAACCCC ACGGGCATCG GGGCCCCAGC CCTGTCCCAG	420
CTGCAGGGAC AGGAGCAGCA GGGAGCCAG CAGGAACCTTC CCTACGGCCA T	471

## (2) INFORMATION FOR SEQ ID NO:207:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 69 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

ATGGCCGTAG GGAAGTCCT GCTGGCTCT CTGCTGCTCC TGTCCCTGCA GCTGGGACAG	60
GGCTGGGGC	69

## (2) INFORMATION FOR SEQ ID NO:208:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 69 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

CCCCCAGCCC TGTCCCAGCT GCAGGGACAG GAGCAGCAGA GAGCCCAGCA GGAACTTCCC	60
TACGGCCAT	69

## (2) INFORMATION FOR SEQ ID NO:209:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 69 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

ATGGCCGTAG GGAAGTTCTCT GCTGGGCTCC CTGCTGCTCC TGTCCTGCA GCTGGGACAG	60
GGCTGGGGC	69

## (2) INFORMATION FOR SEQ ID NO:210:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 69 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

CCCCCAGCCC TGTCCCAGCT GCAGGGACAG GAGCAGCAGG GAGCCCAGCA GGAACTTCCC	60
TACGGCCAT	69

## (2) INFORMATION FOR SEQ ID NO:211:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 111 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

CCCGATGCC	GTGGGTTCC	CGTGGCCGAT	GGAGAGTTCT	CGTCTGAACA	GGTGGCAAAG	60
GCTGGAGGGA	CCTGGCTGGG	CACCCACCGC	CCCCTTGCCC	GCCTGCGCCG	A	111

(2) INFORMATION FOR SEQ ID NO:211:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 111 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

TCGGCGCAGG	CGGGCAAGGG	GGCGGTGGGT	GCCCCAGCCAG	GTCCCTCCAG	CCTTTGCCAC	60
CTGTTCA	GAGAACTCTC	CATCGGCCAC	GGGAACCCCA	CGGGCATCGG	G	111

(2) INFORMATION FOR SEQ ID NO:212:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 180 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

ATGGCCGTAG	GGAAAGTTCT	GCTGGGCTCT	CTGCTGCTCC	TGTCCCTGCA	GCTGGGACAG	60
GGCTGGGGCC	CCGATGCCCG	TGGGGTTCCC	GTGGCCGATG	GAGAGTTCTC	GTCTGAACAG	120
GTGGCAAAGG	CTGGAGGGAC	CTGGCTGGGC	ACCCACCGCC	CCCTTGCCCG	CCTGCGCCGA	180

(2) INFORMATION FOR SEQ ID NO:213:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 180 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

TCGGCGCAGG CGGGCAAGGG GGCGGTGGGT GCCCAGCCAG GTCCCTCCAG CCTTTGCCAC	60
CTGTTCAGAC GAGAACTCTC CATCGGCCAC GGGAACCCCA CGGGCATCGG GGCCCCAGCC	120
CTGTCCCAGC TGCAGGGACA GGAGCAGCAG AGAGCCCAGC AGGAACTTCC CTACGGCCAT	180

## (2) INFORMATION FOR SEQ ID NO:215:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 180 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

ATGGCCGTAG GGAAGTTCTT GCTGGGCTCC CTGCTGCTCC TGTCCTGCA GCTGGGACAG	60
GGCTGGGGCC CCGATGCCCG TGGGGTTCCC GTGGCCGATG GAGAGTTCTC GTCTGAACAG	120
GTGGCAAAGG CTGGAGGGAC CTGGCTGGGC ACCCACCGCC CCCTTGCCCG CCTGCGCCGA	180

## (2) INFORMATION FOR SEQ ID NO:216:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 180 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

TCGGCGCAGG CGGGCAAGGG GGCGGTGGGT GCCCAGCCAG GTCCCTCCAG CCTTTGCCAC	60
CTGTTCAGAC GAGAACTCTC CATCGGCCAC GGGAACCCCA CGGGCATCGG GGCCCCAGCC	120
CTGTCCCAGC TGCAGGGACA GGAGCAGCAG GGAGCCCAGC AGGAACTTCC CTACGGCCAT	180

## (2) INFORMATION FOR SEQ ID NO:217:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 156 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

Met Ala Val Gly Lys Phe Leu Leu Gly Ser Leu Leu Leu Leu Ser Leu	
1 5 10 15	

Gln Leu Gly Gln Gly Trp Gly Pro Asp Ala Arg Gly Val Pro Val Ala  
 20 25 30

Asp Gly Glu Phe Ser Ser Glu Gln Val Ala Lys Ala Gly Gly Thr Trp  
 35 40 45

Leu Gly Thr His Arg Pro Leu Ala Arg Leu Arg Arg Ala Leu Ser Gly  
 50 55 60

Pro Cys Gln Leu Trp Ser Leu Thr Leu Ser Val Ala Glu Leu Gly Leu  
 65 70 75 80

Gly Tyr Ala Ser Glu Glu Lys Val Ile Phe Arg Tyr Cys Ala Gly Ser  
 85 90 95

Cys Pro Arg Gly Ala Arg Thr Gln His Gly Leu Ala Leu Ala Arg Leu  
 100 105 110

Gln Gly Gln Gly Arg Ala His Gly Gly Pro Cys Cys Arg Pro Thr Arg  
 115 120 125

Tyr Thr Asp Val Ala Phe Leu Asp Asp Arg His Arg Trp Gln Arg Leu  
 130 135 140

Pro Gln Leu Ser Ala Ala Cys Gly Cys Gly Gly  
 145 150 155

## (2) INFORMATION FOR SEQ ID NO:218:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 60 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

Met Ala Val Gly Lys Phe Leu Leu Gly Ser Leu Leu Leu Leu Ser Leu  
 1 5 10 15

Gln Leu Gly Gln Gly Trp Gly Pro Asp Ala Arg Gly Val Pro Val Ala  
 20 25 30

Asp Gly Glu Phe Ser Ser Glu Gln Val Ala Lys Ala Gly Gly Thr Trp  
 35 40 45

Leu Gly Thr His Arg Pro Leu Ala Arg Leu Arg Arg  
 50 55 60

## (2) INFORMATION FOR SEQ ID NO:219:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

Met Ala Val Gly Lys Phe Leu Leu Gly Ser Leu Leu Leu Ser Leu			
1	5	10	15
Gln Leu Gly Gln Gly Trp Gly			
20			

## (2) INFORMATION FOR SEQ ID NO:220:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
  
- (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

Pro Asp Ala Arg Gly Val Pro Val Ala Asp Gly Glu Phe Ser Ser Glu			
1	5	10	15
Gln Val Ala Lys Ala Gly Gly Thr Trp Leu Gly Thr His Arg Pro Leu			
20	25	30	
Ala Arg Leu Arg Arg			
35			

## (2) INFORMATION FOR SEQ ID NO:221:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 96 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
  
- (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

Ala Leu Ser Gly Pro Cys Gln Leu Trp Ser Leu Thr Leu Ser Val Ala			
1	5	10	15
Glu Leu Gly Leu Gly Tyr Ala Ser Glu Glu Lys Val Ile Phe Arg Tyr			
20	25	30	
Cys Ala Gly Ser Cys Pro Arg Gly Ala Arg Thr Gln His Gly Leu Ala			
35	40	45	
Leu Ala Arg Leu Gln Gly Gln Gly Arg Ala His Gly Gly Pro Cys Cys			
50	55	60	
Arg Pro Thr Arg Tyr Thr Asp Val Ala Phe Leu Asp Asp Arg His Arg			
65	70	75	80
Trp Gln Arg Leu Pro Gln Leu Ser Ala Ala Cys Gly Cys Gly Gly			
85	90	95	

## (2) INFORMATION FOR SEQ ID NO:222:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 267 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

TGCCAGCTGT GGAGCCTGAC CCTGTCCGTG GCAGAGCTAG GCCTGGGCTA CGCCTCAGAG	60
GAGAAGGTCA TCTTCCGCTA CTGCGCCGGC AGCTGCCCCC GTGGTGCCCC CACCCAGCAT	120
GGCCTGGCGC TGGCCCGGCT GCAGGGCCAG GGCCGAGCCC ACGGTGGGCC CTGCTGCCGG	180
CCCACTCGCT ACACCGACGT GGCCCTCCTC GATGACCGCC ACCGCTGGCA GCGGCTGCC	240
CAGCTCTCGG CGGCTGCCTG CGGCTGT	267

## (2) INFORMATION FOR SEQ ID NO:223:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 89 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

Cys Gln Leu Trp Ser Leu Thr Leu Ser Val Ala Glu Leu Gly Leu Gly	
1 5 10 15	
Tyr Ala Ser Glu Glu Lys Val Ile Phe Arg Tyr Cys Ala Gly Ser Cys	
20 25 30	
Pro Arg Gly Ala Arg Thr Gln His Gly Leu Ala Leu Ala Arg Leu Gln	
35 40 45	
Gly Gln Gly Arg Ala His Gly Gly Pro Cys Cys Arg Pro Thr Arg Tyr	
50 55 60	
Thr Asp Val Ala Phe Leu Asp Asp Arg His Arg Trp Gln Arg Leu Pro	
65 70 75 80	
Gln Leu Ser Ala Ala Ala Cys Gly Cys	
85	

## (2) INFORMATION FOR SEQ ID NO:224:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 5 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

Ala Leu Ser Gly Pro  
1               5

(2) INFORMATION FOR SEQ ID NO:225:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

GTSASYGASY TGGGYCTGGG CTAY

24

(2) INFORMATION FOR SEQ ID NO:226:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

TTYMGSTACT GCRSMGGCKC YTGC

24

(2) INFORMATION FOR SEQ ID NO:227:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

RWAGGCSRTS GGKCKGCARC AKGS

24

(2) INFORMATION FOR SEQ ID NO:228:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

MKCRTCYARR AASGACASST C

21

(2) INFORMATION FOR SEQ ID NO:229:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 168 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

CGGCTTGTGA CCGAGCTGGG CCTGGGCTAC GCCTCAGAGG AGAAGGTCAT CTTCCGCTAC

60

TGCGCCGGCA GCTGCCCGG TGGTGCCCCGC ACCCAGCATG GCCTGGCGCT GGCCCGGCTG

120

CAGGGGCCAGG GCCGAGCCCA CGGCAGGGCCC TGCTGCCGCC CCATGGCC

168

(2) INFORMATION FOR SEQ ID NO:230:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

GAGGAGAAAGG TCATCTTCCG

20

(2) INFORMATION FOR SEQ ID NO:231:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

GCCGTGGGCT CGGCCCTGGC

20

## (2) INFORMATION FOR SEQ ID NO:232:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:

AGAGGGAGAAG GTCATCTTCC GCTA

24

## (2) INFORMATION FOR SEQ ID NO:233:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:

CTCGGCCCTG GCCCTGCAGC

20

## (2) INFORMATION FOR SEQ ID NO:234:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:

TGCAGCCGGG CCAGCGCCAG

20

## (2) INFORMATION FOR SEQ ID NO:235:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 31 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:

CGCGGATCCA TGCCTGGATT CGAGGGTGCA G 31

(2) INFORMATION FOR SEQ ID NO:236:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 31 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:

CGCGGATCCA TGGCCGTAGG GAAGTTCCCTG C 31

(2) INFORMATION FOR SEQ ID NO:237:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 60 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237:

CTCCCAAGCT TTTACTTGTC ATCGTCGTCC TTGTAGTCGC CACCACAGCC GCAGGCAGCC 60

(2) INFORMATION FOR SEQ ID NO:238:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 59 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:

CTCCCAAGCT TTTACTTGTC ATCGTCGTCC TTGTAGTCTC GAGGAAGGCC ACGTCGGTG 59

(2) INFORMATION FOR SEQ ID NO:239:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:  
 TCAGGCCACCA CAGCCGCAGG CAGCC

25

## (2) INFORMATION FOR SEQ ID NO:240:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 73 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:

Ser	Glu	Glu	Lys	Ile	Ile	Phe	Arg	Tyr	Cys	Ala	Gly	Ser	Cys	Pro
5									10					15

  

Gln	Glu	Val	Arg	Thr	Gln	His	Ser	Leu	Val	Leu	Ala	Arg	Leu	Arg
20									25					30

  

Gly	Gln	Gly	Arg	Ala	His	Gly	Arg	Pro	Cys	Cys	Gln	Pro	Thr	Ser
35									40					45

  

Tyr	Ala	Asp	Val	Thr	Phe	Leu	Asp	Asp	His	His	His	Trp	Gln	Gln
50									55					60

  

Leu	Pro	Gln	Leu	Ser	Ala	Ala	Ala	Cys	Gly	Cys	Gly	Gly		
65									70					

## (2) INFORMATION FOR SEQ ID NO:241:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 93 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

Cys	Val	Leu	Thr	Ala	Ile	His	Leu	Asn	Val	Thr	Asp	Leu	Gly	Leu
5									10					15

  

Gly	Tyr	Glu	Thr	Lys	Glu	Glu	Leu	Ile	Phe	Arg	Tyr	Cys	Ser	Gly
20									25					30

  

Ser	Cys	Glu	Ala	Ala	Glu	Thr	Met	Tyr	Asp	Lys	Ile	Leu	Lys	Asn
35									40					45

Leu Ser Arg Ser Arg Arg Leu Thr Ser Asp Lys Val Gly Gln Ala  
 50 55 60  
 Cys Cys Arg Pro Val Ala Phe Asp Asp Asp Leu Ser Phe Leu Asp  
 65 70 75  
 Asp Ser Leu Val Tyr His Ile Leu Arg Lys His Ser Ala Lys Arg  
 80 85 90  
 Cys Gly Cys

## (2) INFORMATION FOR SEQ ID NO:242:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 93 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:

Cys Val Leu Thr Ala Ile His Leu Asn Val Thr Asp Leu Gly Leu Gly  
 5 10 15  
 Tyr Glu Thr Lys Glu Glu Leu Ile Phe Arg Tyr Cys Ser Gly Ser Cys  
 20 25 30  
 Glu Ser Ala Glu Thr Met Tyr Asp Lys Ile Leu Lys Asn Leu Ser Arg  
 35 40 45  
 Ser Arg Arg Leu Thr Ser Asp Lys Val Gly Gln Ala Cys Cys Arg Pro  
 50 55 60  
 Val Ala Phe Asp Asp Asp Leu Ser Phe Leu Asp Asp Asn Leu Val Tyr  
 65 70 75 80  
 His Ile Leu Arg Lys His Ser Ala Lys Arg Cys Gly Cys  
 85 90

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